



## SEQUENCE LISTING

Levin, Joshua Z.  
Budziszewski, Gregory J.  
Potter, Sharon L.  
Wegrich, Lynette M.

<120> Herbicide Target Genes and Methods

<130> PB/5-30780DIV

<140> 10/047,412

<141> 2002/01/14

<160> 29

<170> PatentIn Ver. 2.1

<210> 1

<211> 1119

<212> DNA

<213> Arabidopsis thaliana

<220>

<221> CDS

<222> (1)..(1119)

<400> 1

atg gat gac atg gac acc gtc tac aag caa ttg gga ttg ttt tca cta	48
Met Asp Asp Met Asp Thr Val Tyr Lys Gln Leu Gly Leu Phe Ser Leu	
1 5 10 15	
aag aag aag att aaa gat gtt gtt ctt aag gct gag atg ttt gca ccg	96
Lys Lys Lys Ile Lys Asp Val Val Leu Lys Ala Glu Met Phe Ala Pro	
20 25 30	
gat gct ctt gag ctt gaa gaa gag cag tgg ata aag caa gaa gaa aca	144
Asp Ala Leu Glu Leu Glu Glu Glu Gln Trp Ile Lys Gln Glu Glu Thr	
35 40 45	
atg cgt tac ttt gat tta tgg gat gat ccc gct aaa tct gat gag att	192
Met Arg Tyr Phe Asp Leu Trp Asp Asp Pro Ala Lys Ser Asp Glu Ile	
50 55 60	
ctt ctc aaa tta gct gat cga gct aaa gca gtc gat tcc ctc aaa gac	240
Leu Leu Lys Leu Ala Asp Arg Ala Lys Ala Val Asp Ser Leu Lys Asp	
65 70 75 80	
ctc aaa tac aag gct gaa gaa gct aag ctg atc ata caa ttg ggt gag	288
Leu Lys Tyr Lys Ala Glu Glu Ala Lys Leu Ile Ile Gln Leu Gly Glu	
85 90 95	
atg gat gct ata gat tac agt ctc ttt gag caa gcc tat gat tca tca	336
Met Asp Ala Ile Asp Tyr Ser Leu Phe Glu Gln Ala Tyr Asp Ser Ser	
100 105 110	
ctc gat gta agt aga tcg ttg cat cac tat gag atg tct aag ctt ctt	384
Leu Asp Val Ser Arg Ser Leu His His Tyr Glu Met Ser Lys Leu Leu	
115 120 125	
agg gat caa tat gac gct gaa ggc gct tgt atg att atc aaa tct gga	432
Arg Asp Gln Tyr Asp Ala Glu Gly Ala Cys Met Ile Ile Lys Ser Gly	
130 135 140	

tct cca ggc gca aaa tct cag ata tgg aca gag caa gtt gta agt atg Ser Pro Gly Ala Lys Ser Gln Ile Trp Thr Glu Gln Val Val Ser Met 145 150 155 160	480
tat atc aaa tgg gca gaa agg cta ggc caa aac gcg cgg gtg gct gag Tyr Ile Lys Trp Ala Glu Arg Leu Gly Gln Asn Ala Arg Val Ala Glu 165 170 175	528
aaa tgt agt tta ttg agt aat aaa agt ggc gta agt tca gcc acg ata Lys Cys Ser Leu Leu Ser Asn Lys Ser Gly Val Ser Ser Ala Thr Ile 180 185 190	576
gag ttt gaa ttc gag ttt gct tat ggt tat ctc tta ggt gag cga ggt Glu Phe Glu Phe Glu Phe Ala Tyr Gly Tyr Leu Leu Gly Glu Arg Gly 195 200 205	624
gtg cac cgc ctt atc ata agt tcc act tct aat gag gaa tgt tca gcg Val His Arg Leu Ile Ile Ser Ser Thr Ser Asn Glu Glu Cys Ser Ala 210 215 220	672
act gtt gat atc ata cca cta ttc ttg aga gca tct cct gat ttt gaa Thr Val Asp Ile Ile Pro Leu Phe Leu Arg Ala Ser Pro Asp Phe Glu 225 230 235 240	720
gta aag gaa ggt gat ttg att gta tcg tat cct gca aaa gag gat cac Val Lys Glu Gly Asp Leu Ile Val Ser Tyr Pro Ala Lys Glu Asp His 245 250 255	768
aaa ata gct gag aat atg gtt tgt atc cac cat att ccg agt gga gta Lys Ile Ala Glu Asn Met Val Cys Ile His His Ile Pro Ser Gly Val 260 265 270	816
aca cta caa tct tca gga gaa aga aac cgg ttt gca aac agg atc aaa Thr Leu Gln Ser Ser Gly Glu Arg Asn Arg Phe Ala Asn Arg Ile Lys 275 280 285	864
gct cta aac cgg ttg aag gcg aag cta ctt gtg ata gca aaa gag caa Ala Leu Asn Arg Leu Lys Ala Lys Leu Leu Val Ile Ala Lys Glu Gln 290 295 300	912
aag gtt tcg gat gta aat aaa atc gac agc aag aac att ttg gaa ccg Lys Val Ser Asp Val Asn Lys Ile Asp Ser Lys Asn Ile Leu Glu Pro 305 310 315 320	960
cgg gaa gaa acc agg agt tat gtc tct aag ggt cac aag atg gtg gtt Arg Glu Glu Thr Arg Ser Tyr Val Ser Lys Gly His Lys Met Val Val 325 330 335	1008
gat aga aaa acc ggt tta gag att ctg gac ctg aaa tcg gtc ttg gat Asp Arg Lys Thr Gly Leu Glu Ile Leu Asp Leu Lys Ser Val Leu Asp 340 345 350	1056
gga aac att gga cca ctc ctt gga gct cat att agc atg aga aga tca Gly Asn Ile Gly Pro Leu Leu Gly Ala His Ile Ser Met Arg Arg Ser 355 360 365	1104
att gat gcg att tag Ile Asp Ala Ile 370	1119

<210> 2  
<211> 372  
<212> PRT

<213> Arabidopsis thaliana

<400> 2

Met Asp Asp Met Asp Thr Val Tyr Lys Gln Leu Gly Leu Phe Ser Leu  
1 5 10 15  
Lys Lys Lys Ile Lys Asp Val Val Leu Lys Ala Glu Met Phe Ala Pro  
20 25 30  
Asp Ala Leu Glu Leu Glu Glu Gln Trp Ile Lys Gln Glu Glu Thr  
35 40 45  
Met Arg Tyr Phe Asp Leu Trp Asp Asp Pro Ala Lys Ser Asp Glu Ile  
50 55 60  
Leu Leu Lys Leu Ala Asp Arg Ala Lys Ala Val Asp Ser Leu Lys Asp  
65 70 75 80  
Leu Lys Tyr Lys Ala Glu Glu Ala Lys Leu Ile Ile Gln Leu Gly Glu  
85 90 95  
Met Asp Ala Ile Asp Tyr Ser Leu Phe Glu Gln Ala Tyr Asp Ser Ser  
100 105 110  
Leu Asp Val Ser Arg Ser Leu His His Tyr Glu Met Ser Lys Leu Leu  
115 120 125  
Arg Asp Gln Tyr Asp Ala Glu Gly Ala Cys Met Ile Ile Lys Ser Gly  
130 135 140  
Ser Pro Gly Ala Lys Ser Gln Ile Trp Thr Glu Gln Val Val Ser Met  
145 150 155 160  
Tyr Ile Lys Trp Ala Glu Arg Leu Gly Gln Asn Ala Arg Val Ala Glu  
165 170 175  
Lys Cys Ser Leu Leu Ser Asn Lys Ser Gly Val Ser Ser Ala Thr Ile  
180 185 190  
Glu Phe Glu Phe Glu Phe Ala Tyr Gly Tyr Leu Leu Gly Glu Arg Gly  
195 200 205  
Val His Arg Leu Ile Ile Ser Thr Ser Asn Glu Glu Cys Ser Ala  
210 215 220  
Thr Val Asp Ile Ile Pro Leu Phe Leu Arg Ala Ser Pro Asp Phe Glu  
225 230 235 240  
Val Lys Glu Gly Asp Leu Ile Val Ser Tyr Pro Ala Lys Glu Asp His  
245 250 255  
Lys Ile Ala Glu Asn Met Val Cys Ile His His Ile Pro Ser Gly Val  
260 265 270  
Thr Leu Gln Ser Ser Gly Glu Arg Asn Arg Phe Ala Asn Arg Ile Lys  
275 280 285  
Ala Leu Asn Arg Leu Lys Ala Lys Leu Leu Val Ile Ala Lys Glu Gln  
290 295 300  
Lys Val Ser Asp Val Asn Lys Ile Asp Ser Lys Asn Ile Leu Glu Pro  
305 310 315 320  
Arg Glu Glu Thr Arg Ser Tyr Val Ser Lys Gly His Lys Met Val Val  
325 330 335  
Asp Arg Lys Thr Gly Leu Glu Ile Leu Asp Leu Lys Ser Val Leu Asp  
340 345 350  
Gly Asn Ile Gly Pro Leu Leu Gly Ala His Ile Ser Met Arg Arg Ser  
355 360 365  
Ile Asp Ala Ile  
370

<210> 3

<211> 1458

<212> DNA

<213> Arabidopsis thaliana

<220>

<221> CDS

<222> (1)..(1458)

<400> 3

atg gca act ctt gaa gat tct ttc ctt gct gat ttg gac gag tta tct Met Ala Thr Leu Glu Asp Ser Phe Leu Ala Asp Leu Asp Glu Leu Ser 1 5 10 15	48
gac aat gaa gca gaa ttg gac gag aat gat ggt gat gtt gga aag gaa Asp Asn Glu Ala Glu Leu Asp Glu Asn Asp Gly Asp Val Gly Lys Glu 20 25 30	96
gaa gaa gat gtt gat atg gat atg gct gat tta gag aca ctt aac tat Glu Glu Asp Val Asp Met Asp Met Ala Asp Leu Glu Thr Leu Asn Tyr 35 40 45	144
gat gat ctc gat aat gtt tct aag ctg cag aag agt cag aga tat gct Asp Asp Leu Asp Asn Val Ser Lys Leu Gln Lys Ser Gln Arg Tyr Ala 50 55 60	192
gat att atg cat aaa gta gag gag gct ctt ggg aaa gat tct gat gga Asp Ile Met His Lys Val Glu Glu Ala Leu Gly Lys Asp Ser Asp Gly 65 70 75 80	240
gct gag aaa gga act gtc ttg gaa gat gat cct gag tat aag ctt att Ala Glu Lys Gly Thr Val Leu Glu Asp Asp Pro Glu Tyr Lys Leu Ile 85 90 95	288
gtg gat tgt aat cag ctt tcg gtc gat att gag aat gaa atc gtt att Val Asp Cys Asn Gln Leu Ser Val Asp Ile Glu Asn Glu Ile Val Ile 100 105 110	336
gtc cac aac ttt atc aaa gac aag tac aag ctt aag ttt caa gag ctt Val His Asn Phe Ile Lys Asp Lys Tyr Lys Leu Lys Phe Gln Glu Leu 115 120 125	384
gag tcg ttg gtt cat cac cct att gac tat gca tgt gtt gtg aag aag Glu Ser Leu Val His His Pro Ile Asp Tyr Ala Cys Val Val Lys Lys 130 135 140	432
att ggg aat gag acg gat ttg gct ctt gtt gat ctc gct gac ctt ctt Ile Gly Asn Glu Thr Asp Leu Ala Leu Val Asp Leu Ala Asp Leu Leu 145 150 155 160	480
cct tca gct att atc atg gtt gtt tca gtt act gct tta act acg aaa Pro Ser Ala Ile Ile Met Val Val Ser Val Thr Ala Leu Thr Thr Lys 165 170 175	528
ggg agt gca ctg cca gag gat gtt ttg caa aag gtg tta gag gct tgt Gly Ser Ala Leu Pro Glu Asp Val Leu Gln Lys Val Leu Glu Ala Cys 180 185 190	576
gat cgg gct tta gat ctt gat tcc gca agg aag aag gtc ctt gag ttt Asp Arg Ala Leu Asp Leu Asp Ser Ala Arg Lys Lys Val Leu Glu Phe 195 200 205	624
gtt gaa agt aag atg gga tct att gca cct aat ctt tct gct att gtt Val Glu Ser Lys Met Gly Ser Ile Ala Pro Asn Leu Ser Ala Ile Val 210 215 220	672
ggg agt gct gtt gca gcc aaa ctc atg ggg act gct gga ggt ttg tca Gly Ser Ala Val Ala Ala Lys Leu Met Gly Thr Ala Gly Gly Leu Ser 225 230 235 240	720
gca ctt gct aaa atg cct gcg tgt aat gtt caa gtt ctt ggc cac aag Ala Leu Ala Lys Met Pro Ala Cys Asn Val Gln Val Leu Gly His Lys 245 250 255	768

agg aag aac ctt gct ggg ttt tct tct gca acg tct cag tcc cgt gtg Arg Lys Asn Leu Ala Gly Phe Ser Ser Ala Thr Ser Gln Ser Arg Val 260 265 270	816
ggg tat ctg gag cag aca gag att tac caa agc acg cct cct gga ctt Gly Tyr Leu Glu Gln Thr Glu Ile Tyr Gln Ser Thr Pro Pro Gly Leu 275 280 285	864
cag gct cgc gct ggc agg ctc gtg gct gca aaa tca act ttg gca gca Gln Ala Arg Ala Gly Arg Leu Val Ala Ala Lys Ser Thr Leu Ala Ala 290 295 300	912
aga gtt gat gct act aga ggg gat ccg tta ggg ata agt gga aaa gct Arg Val Asp Ala Thr Arg Gly Asp Pro Leu Gly Ile Ser Gly Lys Ala 305 310 315 320	960
ttc agg gag gag atc cgt aag aag att gag aaa tgg caa gaa cct cct Phe Arg Glu Glu Ile Arg Lys Lys Ile Glu Lys Trp Gln Glu Pro Pro 325 330 335	1008
cct gca aga cag cct aag cca ctt cct gtt cct gat tct gaa ccg aag Pro Ala Arg Gln Pro Lys Pro Leu Pro Val Pro Asp Ser Glu Pro Lys 340 345 350	1056
aaa aga agg ggt ggt cgc cgt cta aga aaa atg aaa gaa agg tat caa Lys Arg Arg Gly Gly Arg Arg Leu Arg Lys Met Lys Glu Arg Tyr Gln 355 360 365	1104
gta aca gat atg agg aag ctg gcc aac aga atg gcg ttt ggt aca cct Val Thr Asp Met Arg Lys Leu Ala Asn Arg Met Ala Phe Gly Thr Pro 370 375 380	1152
gaa gag agc tcc ctc ggt gat gga cta gga gaa ggt tat gga atg ctt Glu Glu Ser Ser Leu Gly Asp Gly Leu Gly Glu Gly Tyr Gly Met Leu 385 390 395 400	1200
ggc cag gca gga agc aac agg ctg cga gta tcc agt gtt ccg agc aag Gly Gln Ala Gly Ser Asn Arg Leu Arg Val Ser Ser Val Pro Ser Lys 405 410 415	1248
ctt aag att aat gct aag gtc gcc aaa aag ctt aaa gaa agg cag tat Leu Lys Ile Asn Ala Lys Val Ala Lys Lys Leu Lys Glu Arg Gln Tyr 420 425 430	1296
gcg ggt ggt gcg act acc tct ggt ttg aca tcg agc ctg gct ttc act Ala Gly Gly Ala Thr Thr Ser Gly Leu Thr Ser Ser Leu Ala Phe Thr 435 440 445	1344
cct gtg cag gga ata gag ttg tgc aat cct cag cag gct tta gga tta Pro Val Gln Gly Ile Glu Leu Cys Asn Pro Gln Ala Leu Gly Leu 450 455 460	1392
gga agt ggg act caa agc act tac ttc tca gag tca gga acc ttc tcg Gly Ser Gly Thr Gln Ser Thr Tyr Phe Ser Glu Ser Gly Thr Phe Ser 465 470 475 480	1440
aag ctg aag aag atc taa Lys Leu Lys Lys Ile 485	1458

<210> 4  
<211> 485  
<212> PRT

<213> Arabidopsis thaliana

<400> 4

```

Met Ala Thr Leu Glu Asp Ser Phe Leu Ala Asp Leu Asp Glu Leu Ser
 1      5      10      15
Asp Asn Glu Ala Glu Leu Asp Glu Asn Asp Gly Asp Val Gly Lys Glu
      20      25      30
Glu Glu Asp Val Asp Met Asp Met Ala Asp Leu Glu Thr Leu Asn Tyr
      35      40      45
Asp Asp Leu Asp Asn Val Ser Lys Leu Gln Lys Ser Gln Arg Tyr Ala
      50      55      60
Asp Ile Met His Lys Val Glu Glu Ala Leu Gly Lys Asp Ser Asp Gly
      65      70      75      80
Ala Glu Lys Gly Thr Val Leu Glu Asp Asp Pro Glu Tyr Lys Leu Ile
      85      90      95
Val Asp Cys Asn Gln Leu Ser Val Asp Ile Glu Asn Glu Ile Val Ile
      100      105      110
Val His Asn Phe Ile Lys Asp Lys Tyr Lys Leu Lys Phe Gln Glu Leu
      115      120      125
Glu Ser Leu Val His His Pro Ile Asp Tyr Ala Cys Val Val Lys Lys
      130      135      140
Ile Gly Asn Glu Thr Asp Leu Ala Leu Val Asp Leu Ala Asp Leu Leu
      145      150      155      160
Pro Ser Ala Ile Ile Met Val Val Ser Val Thr Ala Leu Thr Thr Lys
      165      170      175
Gly Ser Ala Leu Pro Glu Asp Val Leu Gln Lys Val Leu Glu Ala Cys
      180      185      190
Asp Arg Ala Leu Asp Leu Asp Ser Ala Arg Lys Lys Val Leu Glu Phe
      195      200      205
Val Glu Ser Lys Met Gly Ser Ile Ala Pro Asn Leu Ser Ala Ile Val
      210      215      220
Gly Ser Ala Val Ala Ala Lys Leu Met Gly Thr Ala Gly Gly Leu Ser
      225      230      235      240
Ala Leu Ala Lys Met Pro Ala Cys Asn Val Gln Val Leu Gly His Lys
      245      250      255
Arg Lys Asn Leu Ala Gly Phe Ser Ser Ala Thr Ser Gln Ser Arg Val
      260      265      270
Gly Tyr Leu Glu Gln Thr Glu Ile Tyr Gln Ser Thr Pro Pro Gly Leu
      275      280      285
Gln Ala Arg Ala Gly Arg Leu Val Ala Ala Lys Ser Thr Leu Ala Ala
      290      295      300
Arg Val Asp Ala Thr Arg Gly Asp Pro Leu Gly Ile Ser Gly Lys Ala
      305      310      315      320
Phe Arg Glu Glu Ile Arg Lys Lys Ile Glu Lys Trp Gln Glu Pro Pro
      325      330      335
Pro Ala Arg Gln Pro Lys Pro Leu Pro Val Pro Asp Ser Glu Pro Lys
      340      345      350
Lys Arg Arg Gly Gly Arg Arg Leu Arg Lys Met Lys Glu Arg Tyr Gln
      355      360      365
Val Thr Asp Met Arg Lys Leu Ala Asn Arg Met Ala Phe Gly Thr Pro
      370      375      380
Glu Glu Ser Ser Leu Gly Asp Gly Leu Gly Glu Gly Tyr Gly Met Leu
      385      390      395      400
Gly Gln Ala Gly Ser Asn Arg Leu Arg Val Ser Ser Val Pro Ser Lys
      405      410      415
Leu Lys Ile Asn Ala Lys Val Ala Lys Leu Lys Glu Arg Gln Tyr
      420      425      430
Ala Gly Gly Ala Thr Thr Ser Gly Leu Thr Ser Ser Leu Ala Phe Thr
      435      440      445
Pro Val Gln Gly Ile Glu Leu Cys Asn Pro Gln Gln Ala Leu Gly Leu
      450      455      460
Gly Ser Gly Thr Gln Ser Thr Tyr Phe Ser Glu Ser Gly Thr Phe Ser
      465      470      475      480
Lys Leu Lys Lys Ile

```

<210> 5  
 <211> 1344  
 <212> DNA  
 <213> *Arabidopsis thaliana*

<220>  
 <221> CDS  
 <222> (1)..(1344)

<400> 5  
 atg gag aac ctt acc cta gtt tct tgc tca gct tct tct cca aag ctg 48  
 Met Glu Asn Leu Thr Leu Val Ser Cys Ser Ala Ser Ser Pro Lys Leu  
 1 5 10 15

tta att gga tgc aat ttc act tcc tcg ctg aaa aac cct act ggg ttt 96  
 Leu Ile Gly Cys Asn Phe Thr Ser Ser Leu Lys Asn Pro Thr Gly Phe  
 20 25 30

tct cgt cgg act cct aat att gtc ctc cgg tgt tcc aaa ata tct gcc 144  
 Ser Arg Arg Thr Pro Asn Ile Val Leu Arg Cys Ser Lys Ile Ser Ala  
 35 40 45

tct gct caa tct caa tct ccc tct tcg cgt ccg gag aac act gga gaa 192  
 Ser Ala Gln Ser Gln Ser Pro Ser Arg Pro Glu Asn Thr Gly Glu  
 50 55 60

atc gtg gtt gtg aaa cag aga agc aaa gct ttt gca agt ata ttt tct 240  
 Ile Val Val Val Lys Gln Arg Ser Lys Ala Phe Ala Ser Ile Phe Ser  
 65 70 75 80

tcg agt cgt gat caa cag aca act tct gtt gct tcc cct agt gtg cct 288  
 Ser Ser Arg Asp Gln Gln Thr Thr Ser Val Ala Ser Pro Ser Val Pro  
 85 90 95

gtg cca cca cca tct tca tca acc ata gga tca cca ctt ttc tgg att 336  
 Val Pro Pro Pro Ser Ser Ser Thr Ile Gly Ser Pro Leu Phe Trp Ile  
 100 105 110

ggt gtt ggt gtt ggt cta tca gct ttg ttc tca tat gta act tca aat 384  
 Gly Val Gly Val Gly Leu Ser Ala Leu Phe Ser Tyr Val Thr Ser Asn  
 115 120 125

tta aag aaa tat gca atg caa aca gct atg aag acg atg atg aac caa 432  
 Leu Lys Lys Tyr Ala Met Gln Thr Ala Met Lys Thr Met Met Asn Gln  
 130 135 140

atg aat acg caa aat agc cag ttt aat aat tct gga ttc cca tca gga 480  
 Met Asn Thr Gln Asn Ser Gln Phe Asn Asn Ser Gly Phe Pro Ser Gly  
 145 150 155 160

tca cct ttt ccg ttt cca ttt cct cct caa aca agt cct gct tcc tcg 528  
 Ser Pro Phe Pro Phe Pro Phe Pro Pro Gln Thr Ser Pro Ala Ser Ser  
 165 170 175

cca ttc caa tct caa tcc cag tct tca ggt gct acc gtt gat gtg aca 576  
 Pro Phe Gln Ser Gln Ser Gln Ser Ser Gly Ala Thr Val Asp Val Thr  
 180 185 190

gcg aca aaa gta gag aca cct cct tca act aaa ccg aaa cct aca cct 624  
 Ala Thr Lys Val Glu Thr Pro Pro Ser Thr Lys Pro Lys Pro Thr Pro  
 7

195					200					205									
gca Ala	aag Lys 210	gat Asp	ata Ile	gag Glu	gtg Val	gat Asp 215	aag Lys	cca Pro	agt Ser	gtt Val	gtc Val 220	tta Leu	gag Glu	gca Ala	agc Ser	672			
aaa Lys 225	gag Glu	aag Lys	aaa Lys	gaa Glu	gaa Glu 230	aag Lys	aac Asn	tat Tyr	gcc Ala	ttt Phe 235	gaa Glu	gac Asp	att Ile	tca Ser	ccc Pro 240	720			
gag Glu	gaa Glu	acc Thr	aca Thr	aaa Lys 245	gaa Glu	agc Ser	cca Pro	ttt Phe	agc Ser 250	aac Asn	tat Tyr	gca Ala	gaa Glu	gtc Val 255	tct Ser	768			
gaa Glu	act Thr	aat Asn	tcc Ser 260	ccc Pro	aaa Lys	gaa Glu	act Thr	cgc Arg 265	ttg Leu	ttt Phe	gag Glu	gat Asp	gtc Val 270	ttg Leu	caa Gln	816			
aat Asn	gga Gly	gct Ala 275	ggc Gly	ccg Pro	gca Ala	aat Asn	ggc Gly 280	gcc Ala	act Thr	gct Ala	tca Ser	gag Glu 285	gtt Val	ttt Phe	caa Gln	864			
tct Ser	ttg Leu 290	ggc Gly	ggc Gly	ggg Gly	aaa Lys	gga Gly 295	ggg Gly	ccg Pro	ggc Gly	tta Leu	tct Ser 300	gta Val	gaa Glu	gct Ala	tta Leu	912			
gag Glu 305	aaa Lys	atg Met	atg Met	gaa Glu	gat Asp 310	cca Pro	aca Thr	gtc Val	cag Gln	aag Lys 315	atg Met	gtt Val	tac Tyr	cca Pro	tac Tyr 320	960			
ttg Leu	cct Pro	gag Glu	gag Glu	atg Met 325	agg Arg	aac Asn	cca Pro	gaa Glu	act Thr 330	ttc Phe	aaa Lys	tgg Trp	atg Met	ctt Leu 335	aaa Lys	1008			
aat Asn	cct Pro	cag Gln	tac Tyr 340	cgt Arg	caa Gln	caa Gln	cta Leu	cag Gln 345	gac Asp	atg Met	ttg Leu	aat Asn 350	aat Asn	atg Met	agt Ser	1056			
ggg Gly	agt Ser	ggc Gly 355	gaa Glu	tgg Trp	gac Asp	aag Lys	cga Arg 360	atg Met	aca Thr	gat Asp	aca Thr	ttg Leu 365	aag Lys	aat Asn	ttt Phe	1104			
gac Asp	ctg Leu 370	aat Asn	agt Ser	cct Pro	gaa Glu	gtg Val 375	aag Lys	caa Gln	caa Gln	ttc Phe	aat Asn 380	caa Gln	ata Ile	gga Gly	cta Leu	1152			
act Thr 385	cca Pro	gaa Glu	gaa Glu	gtc Val	ata Ile 390	tct Ser	aag Lys	atc Ile	atg Met	gag Glu 395	aac Asn	cct Pro	gat Asp	gtt Val	gcc Ala 400	1200			
atg Met	gca Ala	ttc Phe	cag Gln 405	aat Asn	cct Pro	aga Arg	gtc Val	caa Gln	gca Ala 410	gca Ala	tta Leu	atg Met	gaa Glu	tgc Cys 415	tca Ser	1248			
gag Glu	aac Asn	cca Pro	atg Met 420	aac Asn	atc Ile	atg Met	aag Lys	tac Tyr 425	caa Gln	aac Asn	gac Asp	aaa Lys	gag Glu 430	gta Val	atg Met	1296			
gat Asp	gtg Val 435	ttc Phe	aac Asn	aag Lys	ata Ile	tcg Ser	cag Gln 440	ctc Leu	ttc Phe	cca Pro	gga Gly 445	atg Met	acg Thr	ggc Gly	tga	1344			



<211> 447  
 <212> PRT  
 <213> Arabidopsis thaliana

<400> 6

Met	Glu	Asn	Leu	Thr	Leu	Val	Ser	Cys	Ser	Ala	Ser	Ser	Pro	Lys	Leu
1				5					10					15	
Leu	Ile	Gly	Cys	Asn	Phe	Thr	Ser	Ser	Leu	Lys	Asn	Pro	Thr	Gly	Phe
			20					25					30		
Ser	Arg	Arg	Thr	Pro	Asn	Ile	Val	Leu	Arg	Cys	Ser	Lys	Ile	Ser	Ala
		35					40					45			
Ser	Ala	Gln	Ser	Gln	Ser	Pro	Ser	Ser	Arg	Pro	Glu	Asn	Thr	Gly	Glu
	50					55					60				
Ile	Val	Val	Val	Lys	Gln	Arg	Ser	Lys	Ala	Phe	Ala	Ser	Ile	Phe	Ser
65					70					75					80
Ser	Ser	Arg	Asp	Gln	Thr	Thr	Ser	Val	Ala	Ser	Pro	Ser	Val	Pro	
			85					90					95		
Val	Pro	Pro	Pro	Ser	Ser	Ser	Thr	Ile	Gly	Ser	Pro	Leu	Phe	Trp	Ile
			100					105					110		
Gly	Val	Gly	Val	Gly	Leu	Ser	Ala	Leu	Phe	Ser	Tyr	Val	Thr	Ser	Asn
		115					120					125			
Leu	Lys	Lys	Tyr	Ala	Met	Gln	Thr	Ala	Met	Lys	Thr	Met	Met	Asn	Gln
	130					135					140				
Met	Asn	Thr	Gln	Asn	Ser	Gln	Phe	Asn	Asn	Ser	Gly	Phe	Pro	Ser	Gly
145					150					155					160
Ser	Pro	Phe	Pro	Phe	Pro	Phe	Pro	Pro	Gln	Thr	Ser	Pro	Ala	Ser	Ser
			165						170					175	
Pro	Phe	Gln	Ser	Gln	Ser	Gln	Ser	Ser	Gly	Ala	Thr	Val	Asp	Val	Thr
		180						185					190		
Ala	Thr	Lys	Val	Glu	Thr	Pro	Pro	Ser	Thr	Lys	Pro	Lys	Pro	Thr	Pro
		195					200					205			
Ala	Lys	Asp	Ile	Glu	Val	Asp	Lys	Pro	Ser	Val	Val	Leu	Glu	Ala	Ser
	210					215					220				
Lys	Glu	Lys	Lys	Glu	Glu	Lys	Asn	Tyr	Ala	Phe	Glu	Asp	Ile	Ser	Pro
225				230						235					240
Glu	Glu	Thr	Thr	Lys	Glu	Ser	Pro	Phe	Ser	Asn	Tyr	Ala	Glu	Val	Ser
			245						250					255	
Glu	Thr	Asn	Ser	Pro	Lys	Glu	Thr	Arg	Leu	Phe	Glu	Asp	Val	Leu	Gln
		260						265					270		
Asn	Gly	Ala	Gly	Pro	Ala	Asn	Gly	Ala	Thr	Ala	Ser	Glu	Val	Phe	Gln
		275					280					285			
Ser	Leu	Gly	Gly	Gly	Lys	Gly	Gly	Pro	Gly	Leu	Ser	Val	Glu	Ala	Leu
	290					295					300				
Glu	Lys	Met	Met	Glu	Asp	Pro	Thr	Val	Gln	Lys	Met	Val	Tyr	Pro	Tyr
305				310						315					320
Leu	Pro	Glu	Glu	Met	Arg	Asn	Pro	Glu	Thr	Phe	Lys	Trp	Met	Leu	Lys
			325						330					335	
Asn	Pro	Gln	Tyr	Arg	Gln	Gln	Leu	Gln	Asp	Met	Leu	Asn	Asn	Met	Ser
		340						345					350		
Gly	Ser	Gly	Glu	Trp	Asp	Lys	Arg	Met	Thr	Asp	Thr	Leu	Lys	Asn	Phe
		355					360					365			
Asp	Leu	Asn	Ser	Pro	Glu	Val	Lys	Gln	Gln	Phe	Asn	Gln	Ile	Gly	Leu
	370					375					380				
Thr	Pro	Glu	Glu	Val	Ile	Ser	Lys	Ile	Met	Glu	Asn	Pro	Asp	Val	Ala
385					390					395					400
Met	Ala	Phe	Gln	Asn	Pro	Arg	Val	Gln	Ala	Ala	Leu	Met	Glu	Cys	Ser
			405						410					415	
Glu	Asn	Pro	Met	Asn	Ile	Met	Lys	Tyr	Gln	Asn	Asp	Lys	Glu	Val	Met
			420					425					430		
Asp	Val	Phe	Asn	Lys	Ile	Ser	Gln	Leu	Phe	Pro	Gly	Met	Thr	Gly	
		435					440					445			

<210> 7  
 <211> 2163  
 <212> DNA  
 <213> Arabidopsis thaliana

<220>  
 <221> CDS  
 <222> (1)..(2163)

<400> 7  
 atg tct agg gag gat ttt agt gat aca ctt cga gta ctt gtt gca act 48  
 Met Ser Arg Glu Asp Phe Ser Asp Thr Leu Arg Val Leu Val Ala Thr  
 1 5 10 15  
 gat tgc cac ttg ggc tac atg gag aag gat gaa att agg cgg cat gat 96  
 Asp Cys His Leu Gly Tyr Met Glu Lys Asp Glu Ile Arg Arg His Asp  
 20 25 30  
 tca ttt aag gct ttc gaa gag ata tgt tct ata gct gag gag aaa cag 144  
 Ser Phe Lys Ala Phe Glu Glu Ile Cys Ser Ile Ala Glu Glu Lys Gln  
 35 40 45  
 gtg gac ttc tta ctc ctc gga ggt gat ctt ttt cat gag aat aaa ccc 192  
 Val Asp Phe Leu Leu Leu Gly Gly Asp Leu Phe His Glu Asn Lys Pro  
 50 55 60  
 tct aga act acg tta gtt aaa gcc att gaa att ctt cgt cgc cac tgt 240  
 Ser Arg Thr Thr Leu Val Lys Ala Ile Glu Ile Leu Arg Arg His Cys  
 65 70 75 80  
 ctg aat gat aaa cca gtg cag ttt caa gta gtc agc gac cag aca gta 288  
 Leu Asn Asp Lys Pro Val Gln Phe Gln Val Val Ser Asp Gln Thr Val  
 85 90 95  
 aat ttt cag aat gcg ttt ggt caa gtc aat tac gag gat cca cac ttc 336  
 Asn Phe Gln Asn Ala Phe Gly Gln Val Asn Tyr Glu Asp Pro His Phe  
 100 105 110  
 aat gta ggc ttg ccc gtg ttc agt att cat gga aac cat gat gat cca 384  
 Asn Val Gly Leu Pro Val Phe Ser Ile His Gly Asn His Asp Asp Pro  
 115 120 125  
 gcc gga gtg gac aat ctt tct gca att gat att ctt tcc gca tgc aac 432  
 Ala Gly Val Asp Asn Leu Ser Ala Ile Asp Ile Leu Ser Ala Cys Asn  
 130 135 140  
 ctt gtg aac tat ttt gga aag atg gtt ctt ggt ggt tct ggt gtt ggc 480  
 Leu Val Asn Tyr Phe Gly Lys Met Val Leu Gly Gly Ser Gly Val Gly  
 145 150 155 160  
 cag att act ctc tac cct ata ctt atg aag aag ggc tca aca acc gtg 528  
 Gln Ile Thr Leu Tyr Pro Ile Leu Met Lys Lys Gly Ser Thr Thr Val  
 165 170 175  
 gct ctc tat ggt tta gga aac atc agg gat gaa cgt ctc aat aga atg 576  
 Ala Leu Tyr Gly Leu Gly Asn Ile Arg Asp Glu Arg Leu Asn Arg Met  
 180 185 190  
 ttt cag acc cca cat gct gtc caa tgg atg agg cct gaa gtt caa gaa 624  
 Phe Gln Thr Pro His Ala Val Gln Trp Met Arg Pro Glu Val Gln Glu  
 195 200 205  
 gga tgt gat gtt tct gac tgg ttc aac att ctg gtg ctt cat caa aat 672  
 Gly Cys Asp Val Ser Asp Trp Phe Asn Ile Leu Val Leu His Gln Asn  
 10

210	215	220	
agg gtg aaa tca aac Arg Val Lys Ser Asn 225	ccc aaa aat gca ata Pro Lys Asn Ala Ile 230	agt gag cac ttt ctt cca Ser Glu His Phe Leu Pro 235	720
cgt ttc ctc gac ttc Arg Phe Leu Asp Phe 245	att gtg tgg ggc cat Ile Val Trp Gly His 250	gag cat gaa tgc cta atc Glu His Glu Cys Leu Ile 255	768
gac ccc cag gag gta tct Asp Pro Gln Glu Val Ser 260	gga atg ggc ttc cac atc Gly Met Gly Phe His Ile 265	aca caa cca gga Thr Gln Pro Gly 270	816
tct tct gtg gca aca tca Ser Ser Val Ala Thr Ser 275	ctt att gat ggg gaa tcg Leu Ile Asp Gly Glu Ser 280	aag cca aaa cat Lys Pro Lys His 285	864
gtt ctt ctc tta gaa atc Val Leu Leu Leu Glu Ile 290	aag gga aat caa tat Lys Gly Asn Gln Tyr 295	cgt cct acg aag ata Arg Pro Thr Lys Ile 300	912
cct ttg aca tct gtg agg Pro Leu Thr Ser Val Arg 305	cct ttt gag tat aca gag Pro Phe Glu Tyr Thr Glu 310	att gtt tta aag Ile Val Leu Lys 315	960
gat gaa agt gat att Asp Glu Ser Asp Ile 325	gat ccc aat gat caa aac Pro Asn Asp Gln Asn Ser 330	tca att ctg gaa cac Ser Ile Leu Glu His 335	1008
ttg gat aaa gtg gtc aga Leu Asp Lys Val Val Arg 340	aat cta ata gag aaa gct Asn Leu Ile Glu Lys Ala 345	agc aaa aaa gct Ser Lys Lys Ala 350	1056
gtt aac aga tca gag atc Val Asn Arg Ser Glu Ile 355	aaa ctc cca ttg gtt cga Lys Leu Pro Leu Val Arg 360	atc aag gta gat Ile Lys Val Asp 365	1104
tat tct gga ttt atg acg Tyr Ser Gly Phe Met Thr 370	ata aat cct caa aga ttt Ile Asn Pro Gln Arg Phe 375	gga cag aaa tat Gly Gln Lys Tyr 380	1152
gtg gga aag gtt gca aat Val Gly Lys Val Ala Asn 385	ccc cag gac att ttg ata Pro Gln Asp Ile Leu Ile 390	ttt tcc aag gct Phe Ser Lys Ala 395	1200
tct aag aag ggt cgg agc Ser Lys Lys Gly Arg Ser 405	gaa gcc aac atc gat gat Glu Ala Asn Ile Asp Asp 410	tct gag cgg ctt Ser Glu Arg Leu 415	1248
cgt cca gaa gaa ctg aac Arg Pro Glu Glu Leu Asn 420	cag cag aat ata gaa gct Gln Gln Asn Ile Glu Ala 425	tta gta gct gaa Leu Val Ala Glu 430	1296
agc aac ctg aaa atg gag Ser Asn Leu Lys Met Glu 435	atc ctt cca gtt aac gat Ile Leu Pro Val Asn Asp 440	ctg gat gtt gct Leu Asp Val Ala 445	1344
ctt cac aat ttt gtg aac Leu His Asn Phe Val Asn 450	aag gat gat aaa cta gcc Lys Asp Asp Lys Leu Ala 455	ttc tac tca tgc Phe Tyr Ser Cys 460	1392
gtt cag tac aat ctt caa Val Gln Tyr Asn Leu Gln 465	gag act cgt ggt aaa ctt Glu Thr Arg Gly Lys Leu 470	gca aag gat tca Ala Lys Asp Ser 475	1440

465	470					475					480					
gat Asp	gcc Ala	aag Lys	aaa Lys	ttt Phe 485	gag Glu	gaa Glu	gat Asp	gac Asp	ttg Leu 490	att Ile	ctt Leu	aaa Lys	gtg Val	gga Gly 495	gag Glu	1488
tgc Cys	tta Leu	gag Glu	gaa Glu 500	cgc Arg	ttg Leu	aaa Lys	gat Asp	agg Arg 505	tcc Ser	act Thr	cga Arg	ccc Pro	act Thr 510	ggt Gly	tcc Ser	1536
tca Ser	cag Gln	ttt Phe 515	tta Leu	tcc Ser	act Thr	gga Gly	ttg Leu 520	act Thr	tca Ser	gag Glu	aat Asn	ttg Leu 525	aca Thr	aaa Lys	gga Gly	1584
agc Ser	agt Ser 530	ggc Gly	atc Ile	gcg Ala	aat Asn	gct Ala 535	tcg Ser	ttc Phe	agt Ser	gat Asp	gat Asp 540	gaa Glu	gac Asp	aca Thr	act Thr	1632
cag Gln 545	atg Met	tct Ser	ggt Gly	tta Leu	gct Ala 550	cct Pro	ccc Pro	act Thr	aga Arg	gga Gly 555	cga Arg	aga Arg	ggt Gly	tca Ser	tcc Ser 560	1680
act Thr	gct Ala	aat Asn	aca Thr	act Thr 565	cgt Arg	ggt Gly	aga Arg	gct Ala	aaa Lys 570	gcc Ala	cca Pro	acc Thr	aga Arg	gga Gly 575	cga Arg	1728
ggc Gly	cgt Arg	ggt Gly	aag Lys 580	gcc Ala	tca Ser	agt Ser	gcg Ala	atg Met 585	aag Lys	caa Gln	acc Thr	act Thr	ctt Leu 590	gat Asp	agt Ser	1776
tct Ser	ctt Leu	ggt Gly 595	ttc Phe	cgc Arg	cag Gln	tct Ser	caa Gln 600	aga Arg	tct Ser	gct Ala	tcg Ser	gct Ala 605	gct Ala	gct Ala	tca Ser	1824
gct Ala 610	gcc Ala	ttc Phe	aaa Lys	agt Ser	gct Ala	tcc Ser 615	acc Thr	att Ile	gga Gly	gaa Glu	gat Asp 620	gat Asp	gta Val	gat Asp	tct Ser	1872
cct Pro 625	tca Ser	agc Ser	gaa Glu	gaa Glu	gtc Val 630	gag Glu	cct Pro	gaa Glu	gat Asp	ttt Phe 635	aac Asn	aaa Lys	cct Pro	gac Asp	agc Ser 640	1920
agt Ser	tcg Ser	gag Glu	gac Asp	gat Asp 645	gag Glu	agc Ser	act Thr	aaa Lys	ggc Gly 650	aaa Lys	gga Gly	cgt Arg	aaa Lys	aga Arg 655	cca Pro	1968
gct Ala	act Thr	act Thr	aag Lys 660	aga Arg	ggc Gly	aga Arg	ggt Gly 665	aga Arg	ggt Gly	tct Ser	ggg Gly	act Thr	tca Ser 670	aaa Lys	cgt Arg	2016
ggt Gly	aga Arg	aaa Lys 675	aac Asn	gaa Glu	agc Ser	tct Ser	tct Ser 680	tca Ser	ctt Leu	aat Asn	agg Arg	cta Leu 685	ctc Leu	agt Ser	agc Ser	2064
aaa Lys	gac Asp 690	gat Asp	gac Asp	gag Glu	gac Asp	gaa Glu 695	gat Asp	gat Asp	gaa Glu	gac Asp	aga Arg 700	gaa Glu	aag Lys	aag Lys	ctt Leu	2112
aac Asn 705	aaa Lys	tct Ser	cag Gln	cct Pro	cgg Arg 710	gtt Val	aca Thr	agg Arg	aac Asn	tat Tyr 715	gga Gly	gct Ala	cta Leu	aga Arg	aga Arg 720	2160
taa																2163

<210> 8  
 <211> 720  
 <212> PRT  
 <213> Arabidopsis thaliana

<400> 8

Met	Ser	Arg	Glu	Asp	Phe	Ser	Asp	Thr	Leu	Arg	Val	Leu	Val	Ala	Thr
1				5					10					15	
Asp	Cys	His	Leu	Gly	Tyr	Met	Glu	Lys	Asp	Glu	Ile	Arg	Arg	His	Asp
			20					25					30		
Ser	Phe	Lys	Ala	Phe	Glu	Glu	Ile	Cys	Ser	Ile	Ala	Glu	Glu	Lys	Gln
		35					40					45			
Val	Asp	Phe	Leu	Leu	Leu	Gly	Gly	Asp	Leu	Phe	His	Glu	Asn	Lys	Pro
	50					55					60				
Ser	Arg	Thr	Thr	Leu	Val	Lys	Ala	Ile	Glu	Ile	Leu	Arg	Arg	His	Cys
65					70					75				80	
Leu	Asn	Asp	Lys	Pro	Val	Gln	Phe	Gln	Val	Val	Ser	Asp	Gln	Thr	Val
				85					90					95	
Asn	Phe	Gln	Asn	Ala	Phe	Gly	Gln	Val	Asn	Tyr	Glu	Asp	Pro	His	Phe
			100					105					110		
Asn	Val	Gly	Leu	Pro	Val	Phe	Ser	Ile	His	Gly	Asn	His	Asp	Asp	Pro
		115					120					125			
Ala	Gly	Val	Asp	Asn	Leu	Ser	Ala	Ile	Asp	Ile	Leu	Ser	Ala	Cys	Asn
	130					135					140				
Leu	Val	Asn	Tyr	Phe	Gly	Lys	Met	Val	Leu	Gly	Gly	Ser	Gly	Val	Gly
145					150					155				160	
Gln	Ile	Thr	Leu	Tyr	Pro	Ile	Leu	Met	Lys	Lys	Gly	Ser	Thr	Thr	Val
				165					170					175	
Ala	Leu	Tyr	Gly	Leu	Gly	Asn	Ile	Arg	Asp	Glu	Arg	Leu	Asn	Arg	Met
			180					185					190		
Phe	Gln	Thr	Pro	His	Ala	Val	Gln	Trp	Met	Arg	Pro	Glu	Val	Gln	Glu
		195					200					205			
Gly	Cys	Asp	Val	Ser	Asp	Trp	Phe	Asn	Ile	Leu	Val	Leu	His	Gln	Asn
	210					215					220				
Arg	Val	Lys	Ser	Asn	Pro	Lys	Asn	Ala	Ile	Ser	Glu	His	Phe	Leu	Pro
225					230					235				240	
Arg	Phe	Leu	Asp	Phe	Ile	Val	Trp	Gly	His	Glu	His	Glu	Cys	Leu	Ile
				245					250					255	
Asp	Pro	Gln	Glu	Val	Ser	Gly	Met	Gly	Phe	His	Ile	Thr	Gln	Pro	Gly
			260					265					270		
Ser	Ser	Val	Ala	Thr	Ser	Leu	Ile	Asp	Gly	Glu	Ser	Lys	Pro	Lys	His
		275					280					285			
Val	Leu	Leu	Leu	Glu	Ile	Lys	Gly	Asn	Gln	Tyr	Arg	Pro	Thr	Lys	Ile
	290					295					300				
Pro	Leu	Thr	Ser	Val	Arg	Pro	Phe	Glu	Tyr	Thr	Glu	Ile	Val	Leu	Lys
305					310					315				320	
Asp	Glu	Ser	Asp	Ile	Asp	Pro	Asn	Asp	Gln	Asn	Ser	Ile	Leu	Glu	His
				325					330					335	
Leu	Asp	Lys	Val	Val	Arg	Asn	Leu	Ile	Glu	Lys	Ala	Ser	Lys	Lys	Ala
			340					345					350		
Val	Asn	Arg	Ser	Glu	Ile	Lys	Leu	Pro	Leu	Val	Arg	Ile	Lys	Val	Asp
		355					360					365			
Tyr	Ser	Gly	Phe	Met	Thr	Ile	Asn	Pro	Gln	Arg	Phe	Gly	Gln	Lys	Tyr
	370					375					380				
Val	Gly	Lys	Val	Ala	Asn	Pro	Gln	Asp	Ile	Leu	Ile	Phe	Ser	Lys	Ala
385					390					395				400	
Ser	Lys	Lys	Gly	Arg	Ser	Glu	Ala	Asn	Ile	Asp	Asp	Ser	Glu	Arg	Leu
				405					410					415	
Arg	Pro	Glu	Glu	Leu	Asn	Gln	Gln	Asn	Ile	Glu	Ala	Leu	Val	Ala	Glu
			420					425					430		
Ser	Asn	Leu	Lys	Met	Glu	Ile	Leu	Pro	Val	Asn	Asp	Leu	Asp	Val	Ala
		435					440					445			

Leu His Asn Phe Val Asn Lys Asp Asp Lys Leu Ala Phe Tyr Ser Cys  
 450 455 460  
 Val Gln Tyr Asn Leu Gln Glu Thr Arg Gly Lys Leu Ala Lys Asp Ser  
 465 470 475 480  
 Asp Ala Lys Lys Phe Glu Glu Asp Asp Leu Ile Leu Lys Val Gly Glu  
 485 490 495  
 Cys Leu Glu Glu Arg Leu Lys Asp Arg Ser Thr Arg Pro Thr Gly Ser  
 500 505 510  
 Ser Gln Phe Leu Ser Thr Gly Leu Thr Ser Glu Asn Leu Thr Lys Gly  
 515 520 525  
 Ser Ser Gly Ile Ala Asn Ala Ser Phe Ser Asp Asp Glu Asp Thr Thr  
 530 535 540  
 Gln Met Ser Gly Leu Ala Pro Pro Thr Arg Gly Arg Arg Gly Ser Ser  
 545 550 555 560  
 Thr Ala Asn Thr Thr Arg Gly Arg Ala Lys Ala Pro Thr Arg Gly Arg  
 565 570 575  
 Gly Arg Gly Lys Ala Ser Ser Ala Met Lys Gln Thr Thr Leu Asp Ser  
 580 585 590  
 Ser Leu Gly Phe Arg Gln Ser Gln Arg Ser Ala Ser Ala Ala Ala Ser  
 595 600 605  
 Ala Ala Phe Lys Ser Ala Ser Thr Ile Gly Glu Asp Asp Val Asp Ser  
 610 615 620  
 Pro Ser Ser Glu Glu Val Glu Pro Glu Asp Phe Asn Lys Pro Asp Ser  
 625 630 635 640  
 Ser Ser Glu Asp Asp Glu Ser Thr Lys Gly Lys Gly Arg Lys Arg Pro  
 645 650 655  
 Ala Thr Thr Lys Arg Gly Arg Gly Arg Gly Ser Gly Thr Ser Lys Arg  
 660 665 670  
 Gly Arg Lys Asn Glu Ser Ser Ser Ser Leu Asn Arg Leu Leu Ser Ser  
 675 680 685  
 Lys Asp Asp Asp Glu Asp Glu Asp Asp Glu Asp Arg Glu Lys Lys Leu  
 690 695 700  
 Asn Lys Ser Gln Pro Arg Val Thr Arg Asn Tyr Gly Ala Leu Arg Arg  
 705 710 715 720

<210> 9  
 <211> 1434  
 <212> DNA  
 <213> Arabidopsis thaliana

<220>  
 <221> CDS  
 <222> (1)..(1434)

<400> 9  
 atg atg aca tta aac tca cta tct cca gct gaa tcc aaa gct att tct 48  
 Met Met Thr Leu Asn Ser Leu Ser Pro Ala Glu Ser Lys Ala Ile Ser  
 1 5 10 15  
 ttc ttg gat acc tcc agg ttc aat cca atc cct aaa ctc tca ggt ggg 96  
 Phe Leu Asp Thr Ser Arg Phe Asn Pro Ile Pro Lys Leu Ser Gly Gly  
 20 25 30  
 ttt agt ttg agg agg agg gat caa ggg aga ggt ttt gga aaa ggt gtt 144  
 Phe Ser Leu Arg Arg Arg Asp Gln Gly Arg Gly Phe Gly Lys Gly Val  
 35 40 45  
 aag tgt tca gtg aaa gtg cag cag caa caa caa cct cct cca gca tgg 192  
 Lys Cys Ser Val Lys Val Gln Gln Gln Gln Gln Pro Pro Pro Ala Trp  
 50 55 60  
 cct ggg aga gct gtt cct gag gcg cct cgt caa tct tgg gat gga cca 240  
 14

Pro 65	Gly	Arg	Ala	Val	Pro 70	Glu	Ala	Pro	Arg	Gln 75	Ser	Trp	Asp	Gly	Pro 80	
aaa Lys	ccc Pro	atc Ile	tct Ser	atc Ile 85	gtt Val	gga Gly	tct Ser	act Thr	ggg Gly 90	tcc Ser	atc Ile	ggc Gly	act Thr	cag Gln 95	aca Thr	288
ttg Leu	gat Asp	att Ile	gtg Val 100	gct Ala	gag Glu	aat Asn	cct Pro	gac Asp 105	aaa Lys	ttt Phe	aga Arg	gtt Val	gtg Val 110	gct Ala	cta Leu	336
gct Ala	gct Ala	ggg Gly 115	tcg Ser	aat Asn	gtt Val	act Thr	cta Leu 120	ctt Leu	gct Ala	gat Asp	cag Gln	gta Val 125	agg Arg	aga Arg	ttt Phe	384
aag Lys	cct Pro 130	gcg Ala	ttg Leu	gtt Val	gct Ala	gtt Val 135	aga Arg	aac Asn	gag Glu	tca Ser	ctg Leu 140	att Ile	aat Asn	gag Glu	ctt Leu	432
aaa Lys 145	gag Glu	gct Ala	tta Leu	gct Ala	gat Asp 150	ttg Leu	gac Asp	tat Tyr	aaa Lys	ccc Pro 155	gag Glu	att Ile	att Ile	cca Pro	gga Gly 160	480
gag Glu	cta Leu	gga Gly	gtg Val 165	att Ile	gag Glu	gtt Val	gcc Ala	cga Arg	cat His 170	cct Pro	gaa Glu	gct Ala	gta Val	acc Thr 175	gtt Val	528
gtt Val	acc Thr	gga Gly	ata Ile 180	gta Val	ggg Gly	tgt Cys	gcg Ala	gga Gly 185	ctg Leu	aag Lys	cct Pro	acg Thr	gtt Val 190	gct Ala	gca Ala	576
att Ile	gaa Glu	gca Ala 195	gga Gly	aag Lys	gac Asp	att Ile	gct Ala 200	ctt Leu	gca Ala	aac Asn	aaa Lys	gag Glu 205	aca Thr	tta Leu	atc Ile	624
gca Ala 210	ggg Gly	ggg Gly	cct Pro	ttc Phe	gtg Val 215	ctt Leu	ccg Pro	ctt Leu	gcc Ala	aac Asn	aaa Lys 220	cat His	aat Asn	gta Val	aag Lys	672
att Ile 225	ctt Leu	ccg Pro	gca Ala	gat Asp	tca Ser 230	gaa Glu	cat His	tct Ser	gcc Ala	ata Ile 235	ttt Phe	cag Gln	tgt Cys	att Ile	caa Gln 240	720
ggg Gly	ttg Leu	cct Pro	gaa Glu	ggc Gly 245	gct Ala	ctg Leu	cgc Arg	aag Lys	ata Ile 250	atc Ile	ttg Leu	act Thr	gca Ala	tct Ser 255	ggg Gly	768
gga Gly	gct Ala	ttt Phe	agg Arg 260	gat Asp	tgg Trp	cct Pro	gtc Val	gaa Glu 265	aag Lys	cta Leu	aag Lys	gaa Glu	gtt Val 270	aaa Lys	gta Val	816
gcg Ala	gat Asp	gcg Ala 275	ttg Leu	aag Lys	cat His	cca Pro	aac Asn 280	tgg Trp	aac Asn	atg Met	gga Gly	aag Lys 285	aaa Lys	atc Ile	act Thr	864
gtg Val 290	gac Asp	tct Ser	gct Ala	acg Thr	ctt Leu	ttc Phe 295	aac Asn	aag Lys	ggg Gly	ctt Leu	gag Glu 300	gtc Val	att Ile	gaa Glu	gcg Ala	912
cat His 305	tat Tyr	ttg Leu	ttt Phe	gga Gly	gct Ala 310	gag Glu	tat Tyr	gac Asp	gat Asp	ata Ile 315	gag Glu	att Ile	gtc Val	att Ile	cat His 320	960
cct	caa	agt	atc	ata	cat	tcc	atg	att	gaa	aca 15	cag	gat	tca	tct	gtg	1008

Pro	Gln	Ser	Ile	Ile	His	Ser	Met	Ile	Glu	Thr	Gln	Asp	Ser	Ser	Val		
				325					330					335			
ctt	gct	caa	ttg	ggg	ttg	cct	gat	atg	cgt	tta	ccg	att	ctc	tac	acc	1056	
Leu	Ala	Gln	Leu	Gly	Trp	Pro	Asp	Met	Arg	Leu	Pro	Ile	Leu	Tyr	Thr		
			340					345					350				
atg	tca	tg	ccc	gat	aga	gtt	cct	tgt	tct	gaa	gta	act	tg	cct	aga	1104	
Met	Ser	Trp	Pro	Asp	Arg	Val	Pro	Cys	Ser	Glu	Val	Thr	Trp	Pro	Arg		
		355					360					365					
ctt	gac	ctt	tgc	aaa	ctc	ggg	tca	ttg	act	ttc	aag	aaa	cca	gac	aat	1152	
Leu	Asp	Leu	Cys	Lys	Leu	Gly	Ser	Leu	Thr	Phe	Lys	Lys	Pro	Asp	Asn		
	370					375					380						
gtg	aaa	tac	cca	tcc	atg	gat	ctt	gct	tat	gct	gct	gga	cga	gct	gga	1200	
Val	Lys	Tyr	Pro	Ser	Met	Asp	Leu	Ala	Tyr	Ala	Ala	Gly	Arg	Ala	Gly		
385					390			395							400		
ggc	aca	atg	act	gga	gtt	ctc	agc	gcc	gcc	aat	gag	aaa	gct	gtt	gaa	1248	
Gly	Thr	Met	Thr	Gly	Val	Leu	Ser	Ala	Ala	Asn	Glu	Lys	Ala	Val	Glu		
				405				410					415				
atg	ttt	att	gat	gaa	aag	ata	agc	tat	ttg	gat	atc	ttc	aag	gtt	gtg	1296	
Met	Phe	Ile	Asp	Glu	Lys	Ile	Ser	Tyr	Leu	Asp	Ile	Phe	Lys	Val	Val		
			420					425					430				
gaa	tta	aca	tgc	gat	aaa	cat	cga	aac	gag	ttg	gta	aca	tca	ccg	tct	1344	
Glu	Leu	Thr	Cys	Asp	Lys	His	Arg	Asn	Glu	Leu	Val	Thr	Ser	Pro	Ser		
		435					440					445					
ctt	gaa	gag	att	gtt	cac	tat	gac	ttg	tg	gca	cgt	gaa	tat	gcc	gcg	1392	
Leu	Glu	Glu	Ile	Val	His	Tyr	Asp	Leu	Trp	Ala	Arg	Glu	Tyr	Ala	Ala		
	450					455					460						
gat	gtg	cag	ctt	tct	tct	ggg	gct	agg	cca	gtt	cat	gca	tga			1434	
Asp	Val	Gln	Leu	Ser	Ser	Gly	Ala	Arg	Pro	Val	His	Ala					
465					470					475							

<210> 10  
 <211> 477  
 <212> PRT  
 <213> Arabidopsis thaliana

<400>	10																
Met	Met	Thr	Leu	Asn	Ser	Leu	Ser	Pro	Ala	Glu	Ser	Lys	Ala	Ile	Ser		
1				5					10					15			
Phe	Leu	Asp	Thr	Ser	Arg	Phe	Asn	Pro	Ile	Pro	Lys	Leu	Ser	Gly	Gly		
			20					25					30				
Phe	Ser	Leu	Arg	Arg	Arg	Asp	Gln	Gly	Arg	Gly	Phe	Gly	Lys	Gly	Val		
		35					40					45					
Lys	Cys	Ser	Val	Lys	Val	Gln	Gln	Gln	Gln	Gln	Pro	Pro	Pro	Ala	Trp		
	50					55					60						
Pro	Gly	Arg	Ala	Val	Pro	Glu	Ala	Pro	Arg	Gln	Ser	Trp	Asp	Gly	Pro		
65					70					75					80		
Lys	Pro	Ile	Ser	Ile	Val	Gly	Ser	Thr	Gly	Ser	Ile	Gly	Thr	Gln	Thr		
				85					90					95			
Leu	Asp	Ile	Val	Ala	Glu	Asn	Pro	Asp	Lys	Phe	Arg	Val	Val	Ala	Leu		
			100					105					110				
Ala	Ala	Gly	Ser	Asn	Val	Thr	Leu	Leu	Ala	Asp	Gln	Val	Arg	Arg	Phe		
		115					120					125					
Lys	Pro	Ala	Leu	Val	Ala	Val	Arg	Asn	Glu	Ser	Leu	Ile	Asn	Glu	Leu		
	130					135					140						



Lys 145	Glu	Ala	Leu	Ala	Asp 150	Leu	Asp	Tyr	Lys	Pro 155	Glu	Ile	Ile	Pro	Gly 160
Glu	Leu	Gly	Val	Ile 165	Glu	Val	Ala	Arg	His 170	Pro	Glu	Ala	Val	Thr	Val
Val	Thr	Gly	Ile 180	Val	Gly	Cys	Ala	Gly 185	Leu	Lys	Pro	Thr	Val	Ala	Ala
Ile	Glu	Ala	Gly 195	Lys	Asp	Ile	Ala	Leu	Ala	Asn	Lys	Glu	Thr	Leu	Ile
Ala	Gly 210	Gly	Pro	Phe	Val	Leu 215	Pro	Leu	Ala	Asn	Lys 220	His	Asn	Val	Lys
Ile	Leu	Pro	Ala	Asp	Ser 230	Glu	His	Ser	Ala	Ile	Phe	Gln	Cys	Ile	Gln 240
Gly	Leu	Pro	Glu	Gly 245	Ala	Leu	Arg	Lys	Ile 250	Ile	Leu	Thr	Ala	Ser	Gly
Gly	Ala	Phe	Arg 260	Asp	Trp	Pro	Val	Glu 265	Lys	Leu	Lys	Glu	Val	Lys	Val
Ala	Asp	Ala 275	Leu	Lys	His	Pro	Asn 280	Trp	Asn	Met	Gly	Lys 285	Lys	Ile	Thr
Val	Asp 290	Ser	Ala	Thr	Leu	Phe 295	Asn	Lys	Gly	Leu	Glu 300	Val	Ile	Glu	Ala
His 305	Tyr	Leu	Phe	Gly	Ala 310	Glu	Tyr	Asp	Asp	Ile 315	Glu	Ile	Val	Ile	His 320
Pro	Gln	Ser	Ile	Ile 325	His	Ser	Met	Ile	Glu 330	Thr	Gln	Asp	Ser	Ser	Val
Leu	Ala	Gln	Leu 340	Gly	Trp	Pro	Asp	Met 345	Arg	Leu	Pro	Ile	Leu	Tyr	Thr
Met	Ser	Trp 355	Pro	Asp	Arg	Val	Pro 360	Cys	Ser	Glu	Val	Thr 365	Trp	Pro	Arg
Leu	Asp 370	Leu	Cys	Lys	Leu	Gly 375	Ser	Leu	Thr	Phe	Lys 380	Lys	Pro	Asp	Asn
Val	Lys	Tyr	Pro	Ser	Met 390	Asp	Leu	Ala	Tyr	Ala 395	Ala	Gly	Arg	Ala	Gly 400
Gly	Thr	Met	Thr	Gly 405	Val	Leu	Ser	Ala	Ala 410	Asn	Glu	Lys	Ala	Val	Glu
Met	Phe	Ile	Asp 420	Glu	Lys	Ile	Ser	Tyr 425	Leu	Asp	Ile	Phe	Lys 430	Val	Val
Glu	Leu	Thr 435	Cys	Asp	Lys	His	Arg 440	Asn	Glu	Leu	Val	Thr 445	Ser	Pro	Ser
Leu	Glu 450	Glu	Ile	Val	His	Tyr 455	Asp	Leu	Trp	Ala	Arg 460	Glu	Tyr	Ala	Ala
Asp 465	Val	Gln	Leu	Ser	Ser 470	Gly	Ala	Arg	Pro	Val 475	His	Ala			

<210> 11  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:  
 oligonucleotide

<400> 11  
 gcggacatct acatttttga

20

<210> 12  
 <211> 1353  
 <212> DNA  
 <213> Arabidopsis thaliana

<400> 12

gctgggtaag	tagatcgttg	catcactatg	agatgtctaa	gcttcttagg	gatcaatatg	60
acgctgaagg	cgcttgtag	attatcaaat	ctggatctcc	aggcgcaaaa	tctcaggtca	120
gtttcatcat	tctcaaggca	cttacagttt	ccaactcttt	gcttgtaact	tagtttctgt	180
ttgttcttaa	acatatcttg	aggatttgca	gatatggaca	gagcaagttg	taagtatgta	240
tatcaaatgg	gcagaaaggc	taggccaaaa	cgcgcggtg	gctgagaaat	gtagtttatt	300
gagtaataaa	agtggcgtaa	gttcagccac	gatagagttt	gaattcgagt	ttgcttatgg	360
ttatctctta	ggtgagcgag	gtgtgcaccg	ccttatcata	agttccactt	ctaatagagg	420
atacattata	agttataact	ctctttctcg	taactaatca	ctttcgtgtc	cattatcatg	480
gccccggaag	gaattaaaag	aggttttctt	tgcgccagga	atgttcagcg	actgttgata	540
tcataccact	attcttgaga	gcattctctg	atgttgaggt	aaaggaaggt	gatttgattg	600
tatcgtatcc	tgcaaaagag	gatcacaaaa	tagctgagaa	tatggtttgt	atccaccata	660
ttccgagtg	agtaacacta	caatcttcag	gtattcttga	gtgtgttgtt	agttgttaca	720
ctttggttta	ctgcatttta	tgcagattat	ataacatgag	gtttttgatg	caggagaaa	780
aaaccgggtt	gcaaacagga	tcaaagctct	aaaccgggtg	aaaggcgaag	tacttgat	840
agcaaaaag	caaaaaggtt	cggatgtaaa	taaaatcgac	agcaagaaca	ttttggaacc	900
gcgggaagaa	accaggagtt	atgtctctaa	gggtcacaa	atgggtgttg	atagaaaaac	960
cggtttagag	attctggacc	tgaatcggt	cttggatgga	aacattggac	cactccttgg	1020
agctcatatt	agcatgagaa	gatcaattga	tgcgatttag	gcttaatcaa	ttggtacttt	1080
aattgctttt	tgttttgtat	ccaaaaagca	acaaatggtt	gcttggtgtg	gtatatatat	1140
aaccttcttg	tccagaacca	tatatgattc	taaccatcaa	acaaagataa	gaattggtga	1200
ctatgtgcta	tactctacaa	tatcaccatg	aatacttcaa	actagacttt	tgataaat	1260
tgaaacggtt	attaccaata	aaacgaaaac	catgaaactc	ttgttttaat	tatcagattc	1320
gagaaagt	tgtacaaaca	tagctgagaa	ggg			1353

<210> 13  
 <211> 184  
 <212> DNA  
 <213> Arabidopsis thaliana

<400> 13						
gcttaatcaa	ttggtacttt	aattgctttt	tggtttgtat	cccaaaagca	acaaatggkt	60
gcttggtgtg	gtatatatat	aaccttcttg	gccagaacca	tatatgawtc	taaccattaa	120
accaagatta	gaattggtga	ctaaaaaaa	agaaaaaaa	aaaaaaaaa	aaaaaaaaa	180
aaaa						184

<210> 14  
 <211> 2170  
 <212> DNA  
 <213> Arabidopsis thaliana

<400> 14						
atggtaagcg	tttctttaac	tctattttct	tcattgtttc	agttattggc	gattgtattc	60
tctgtttatt	gtaatcgtat	tgtgttaatt	ttgatttgac	tcattcttct	ttaaagttca	120
tttcaaaatt	agggattccg	agatcataga	tattgctttg	tttccgagat	ttgagttatt	180
cttaagcttg	ttttactaac	tttcaatatg	ttggatttgt	tataggcaac	tcttgaagat	240
tctttccttg	ctgatttgga	cgagttatct	gacaatgaag	cagaattggt	gagtgttaaa	300
acacttttga	ttactattat	ctgtttactt	ggaggagcta	tgattgtaat	tgtagtttgt	360
ttgattatac	atatgcagga	cgagaatgat	ggtgatgttg	gaaaggaaga	agaagatggt	420
gatatggata	tggctgattt	agagacactt	aactatgatg	atctcgataa	tgtttctaag	480
ctgcagaaga	gtcagagata	tgctgatatt	atgcataaag	tagaggaggc	tcttgggaaa	540
gattctgatg	gagctgagaa	aggaactgtc	ttggaagatg	atcctgagta	taagcttatt	600
gtggattgta	atcagctttc	ggtcgatatt	gagaatgaaa	tcgttattgt	ccacaacttt	660
atcaaagaca	agtacaagct	taagtttcaa	gagcttgagt	cgttggttca	tcaccctatt	720
gactatgcat	gtgttgtaga	gaagattggg	aatgagacgg	atttggtctt	tggtgatctc	780
gctgaccttc	ttctctcagc	tattatcatg	gtgttttcag	ttactgcttt	aactacgaaa	840
gggaggtcac	tgccagagga	tgttttgcaa	aaggtgttag	aggcttgtag	tcgggcttta	900
gatcttgatt	ccgcaaggaa	gaaggtcctt	gagtttggtg	aaagtaagat	gggatctatt	960
gcacctaatc	tttctgctat	tggtgggagt	gctgttgtag	ccaaactcat	ggggactgct	1020
ggaggtttgt	cagcacttgc	taaaatgcct	gcgtgtaatg	ttcaagttct	tgccacaag	1080
aggaagaacc	ttgctgggtt	ttcttctgca	acgtctcagt	cccgtgtggg	ttatctggag	1140
cagacagaga	tttaccaaa	cacgcctcct	ggacttcagg	ctcgcgtggg	caggctcgtg	1200
gctgcaaaat	caactttggc	agcaagagtt	gatgtacta	gaggggatcc	gttagggata	1260

```

agtggaaaag ctttcaggga ggagatccgt aagaagattg agaaatggca agaaccctcct 1320
cctgcaagac agcctaagcc acttcctgtt cctgattctg aaccgaagaa aagaaggggt 1380
ggtcgccgtc taagaaaaat gaaagaaagg tagccttttt catcctactt tgtgtcctta 1440
attactgtag attgagttct attcacctgt atttattttg ttgcattctt acgtttctct 1500
ttaaatacagg tatcaagtaa cagatatgag gaagctggcc aacagaatgg cgtttggtac 1560
acctgaagag agctccctcg gtaatatatc ttgtagttac acttgtaaat ggccacttat 1620
aaggcactta gtctaataatc tactcttcat gatgataggat gatggactag gagaaggtta 1680
tggaatgctt ggccaggcag gaagcaacag gctgcgagta tccagtgttc cgagcaagct 1740
taagattaat gctaaggctc ccaaaaagta agtggttcctc tatttctcct gtgttttttc 1800
ggatttatca tgttaatat tttactctta caaattatcc tgccctgttc ttcttccatc 1860
atatctcatt tgcgtcttta tatcaattac tttttcaggc ttaaagaaag gcagtatgcg 1920
ggtggtgcga ctacctctgg ttgacatcg agcctggctt tccactcctgt gcagggtacaa 1980
acatttcatt cgattcttga caaaagtttg atcctgtgtt ccatttgcat cactgtctga 2040
ctccaattgg ttatctattt gacagggaa agagttgtgc aatcctcagc aggctttagg 2100
attaggaagt gggactcaaa gcacttactt ctcagagtca ggaaccttct cgaagctgaa 2160
gaagatctaa 2170

```

```

<210> 15
<211> 20
<212> DNA
<213> Artificial Sequence

```

```

<220>
<223> Description of Artificial Sequence:
        oligonucleotide

```

```

<400> 15
accttaggcg acttttgaac 20

```

```

<210> 16
<211> 24
<212> DNA
<213> Artificial Sequence

```

```

<220>
<223> Description of Artificial Sequence:
        oligonucleotide

```

```

<400> 16
aaacgcttac catatctctt tcta 24

```

```

<210> 17
<211> 113
<212> DNA
<213> Arabidopsis thaliana

```

```

<400> 17
aaacactagt cgctcgctgc tcttcaattt tcttctcgaa tctaatacgaat tgattttctcc 60
ttcgattctt caggagaatc actgaagctt ttgcctccca agtagaaaga gat 113

```

```

<210> 18
<211> 218
<212> DNA
<213> Arabidopsis thaliana

```

```

<220>
<221> misc_feature
<222> (1)..(218)
<223> n = a, t, c or g

```

<400> 18

aatatggaag	acagagatnc	aagtcttgaa	aagccgagca	ctaaaagtgt	aaaaatgaac	60
caaaggtgga	aagaaactgc	tttctctatc	tcatgtctgt	tttaagggtt	cttcggtcac	120
ttaagagaca	aaaggcattg	ttttgatcac	tctttggaaa	cgttttataa	attttatttt	180
tgtattagag	ccaaaaaaa	aaaaaaaaa	aaaaaaaaa			218

<210> 19

<211> 4140

<212> DNA

<213> *Arabidopsis thaliana*

<400> 19

cagtacactt	agctacactg	gatccaagtc	tagtgctaaa	ctcaaaccctc	gtgggttttag	60
acaaaaatct	cttcttcttc	gtttctctct	tcctcatcat	atctttcatc	ttctccacca	120
gaatttggtt	taggtctctc	ttcttctgtt	tctttttctc	ccaaagaaac	aattagatat	180
ggagaacctt	accctagttt	cttgctcagc	ttcttctcca	aagctgttaa	ttggatgcaa	240
tttcaacttc	tcgctgaaaa	accctactgg	gttttctcgt	cggactccta	atattgtcct	300
ccggtgttcc	aaaatatctg	cctctgctca	atctcaatct	ccctcttcgc	gtccggagaa	360
cactggagaa	atcggttagt	ttgcaaattc	cactcgacac	tctattatag	caaatgccaa	420
aattttccgg	aaaaatttcc	agtttattac	ttttatctat	cttattgaaa	ctcaaattgc	480
gaaccctttt	cgactgggtt	aatatgagct	tatgaattgc	tatatctctt	aaaaaaatcc	540
acatttggtg	aatttgcaat	ttgaattctt	gtagaaacca	ttcattgtta	gaattgttta	600
ctttaagttt	atgttcgatt	tgcagtgggt	gtgaaacaga	gaagcaaagc	ttttgcaagt	660
atattttctt	cgagtcgtga	tcaacagaca	acttctgttg	cttcccctag	tgtgcctgtg	720
ccaccaccat	cttcatcaac	catgtaattt	tcctgggttt	ggacaatgtg	cttagtttgt	780
atgtcgtttg	attcttggtt	attaaattgt	gttttttctt	ttttcttgta	gaggatcacc	840
acttttctgg	attggtgttg	gtgttggtct	atcagctttg	ttctcatatg	tgagtatcaa	900
gattccttcc	taattttttt	ttcctctata	aatattcttt	cttgcttcaa	tattgattaa	960
taagtgtctt	accttttttc	ttttctgtag	gcatttcagg	taacttcaaa	tttaaaggta	1020
cagatacttg	gccctctggt	tttacgggac	ttttgttctc	tagtctgttg	cagaaccacg	1080
attttatgct	tcatgtcaac	tctagtgtat	tgtgctcatg	tatctgagat	agttttattc	1140
actaaactgg	ttatcttaac	aagggtgaact	gtttgctcac	acttggtgaa	ccgtttatat	1200
aagcatcgaa	cttttgcttc	tctttttttg	ggtagtcact	tgattcgtag	atggtaacct	1260
acataccatt	atggttttag	tgatgcaact	caggatttca	gacttatagt	catttttcga	1320
actccagtat	ttgattgaaa	tatattatac	aagttgtcat	tgctttctct	cattattctc	1380
taaccggctg	ttactctctt	tggatttttt	tttttgcttt	ggtttagaaa	tatgcaatgc	1440
aaacagctat	gaagacgatg	atgaaccaaa	tgaatacgca	aaatagccag	tttaataatt	1500
ctggattccc	atcaggatca	ccttttccgt	ttccatttcc	tcctcaaaca	agtcctgctt	1560
cctcgccatt	ccaatctcaa	tcccagtcct	caggtgctac	cgttgatgtg	acagcgacaa	1620
aagtagagac	acctccttca	actaaaccga	aacctacacc	tgcaaaggat	atagagggtg	1680
ataagccaag	tgttgcttta	gaggcaagca	aagagaagaa	agaagaaaag	aactatggta	1740
gattcttttt	ctgtttcaga	aatcaacgtc	ttttcatttg	tattctcaat	tttgactttc	1800
ttcctttctc	attttccaag	cttctaactt	ggaagctgat	ttacttttgg	atgcagcctt	1860
tgaagacatt	tcacccgagg	aaaccacaaa	agaaagccca	tttagcaact	atgcagaagt	1920
ctctgaaact	aattccccc	aagaaactcg	cttggttgag	gatgtaagtt	tcgttttctt	1980
ttgtatttcc	acagcacacc	aagtgggtgat	ttaaaaacgt	gacatagttt	tgctaacctt	2040
ctatgctctc	ttattgatct	ctgggtgaag	gtcttgcaaa	atggagctgg	tccggcaaat	2100
ggtgccactg	cttcagaggt	ttttcaatct	ttgggtgagt	tattgaattt	cagttttcat	2160
cactatcagc	gcactgtgca	tgattcatga	ttaaggctac	ggatttcaat	tttattttat	2220
agcatatgcc	aacaattata	aacaaaggaa	gatatgaaat	tgggtgataaa	gaggaatgag	2280
ttggcttcaa	aaggatctac	tccgttactt	ttgtccttct	gctagtcggt	gatctgtatt	2340
ggtataacca	tataagactt	gcaggatatt	accttggtca	tctgtttcat	atctcatgtg	2400
ttatgattct	tttttcttat	atgctcacgt	tattgtctct	cttttcctta	ttctaaattt	2460
aaaactgaat	cctgagtcct	tctattgttt	acacaggtgg	tgggaaagga	gggccgggtt	2520
tatctgtaga	agcttttagag	aaaatgatgg	aagatccaac	agtccagaag	atggtttacc	2580
cgtaactcat	cttccctagc	acattgtctt	taaatgcac	cattaagttt	atctttaaaa	2640
ctgggttgctt	agtggacatt	tggtaacatt	gcattgtata	atgcagatac	ttgcctgagg	2700
agatgaggaa	cccgaaaact	ttcaaattga	agctttttta	tatttaattc	tgctatcatt	2760
cttttattag	tcctcatttt	tacatatttc	taaagactaa	aggttacatg	actagctttt	2820
gaatgatgta	attcgtttat	aggttgatcc	aatggttatc	taaatttaaa	atacagtttg	2880
gtacttattg	tctccgcttg	gaattttgta	gggatgctta	aaaatcctca	gtaccgtcaa	2940
caactacagg	acatgtttga	agagctccat	tttacgaaca	atthagttgt	ttccattgct	3000
tttaagaatg	tctaaactat	gtaattaaga	aatactcttg	tttgtttctt	ttcatgaatt	3060

taggaataat	atgagtggga	gtggtgaatg	ggacaagcga	atgacagata	cattgaagaa	3120
ttttgacctg	aatagtcctg	aagtgaagca	acaattcagt	aagacaaatc	tcagtttgta	3180
ccaagttaat	agtacgttaa	ataggctga	tactcaatga	ttgaatctgt	atttgtcaga	3240
tcaaatagga	ctaactccag	aagaagtcac	atctaagatc	atggagaacc	ctgatgttgc	3300
catggcattc	cagaatccta	gagtcacaagc	agcgttaatg	gaagtacgtt	ttcttttaac	3360
ctgaataaga	gaattgctta	attttaccac	acttctttct	tcatacaaaa	cagaaaccaa	3420
ttacattctt	gttggtgttg	cagtgtctcag	agaacccaat	gaacatcatg	aagtaccaa	3480
acgacaaaga	ggtataataa	ctgccacttc	tccattgccc	aaaaaggcga	ttactttttt	3540
aagaaatttg	aggttattat	acattgattg	caggtaatgg	atgtgttcaa	caagatatcg	3600
cagctcttcc	caggaatgac	gggttgaaaa	agctcacgtc	tttggttcta	tcaaaaatgt	3660
cacattgtct	ttagcttttt	gtaggagaa	aaaaatgttt	ttttttttgc	aaagagtctt	3720
cagttttggt	cagatcagag	aattgtgtac	catgttaatc	ttaaacgcgg	tcgggaattg	3780
gagtcgtgtg	aaaacgccgc	tgctgttgtt	tggtatgaat	attatacaat	agaatttggt	3840
gtcttaccaa	aaaaagtcta	tgaagacact	gaagagcaaa	ttattatttt	taagggaaaa	3900
tttccaaaat	aaacttcacg	tattcaaaat	ttgcttgaaa	aaacctcaat	tttttttggt	3960
tgagattgtg	tgaataaatc	tgccaatatt	ttgttttagc	aatttaaaaa	attgaagttt	4020
ttttctcgca	aattttaaat	agttgtgatt	tattttggaa	ttttacctta	tttttaatat	4080
ccaaaaggag	aagtgcagtg	gcgatatcga	agcggtttaa	tgaagtgatg	gccccatctt	4140

<210> 20  
 <211> 77  
 <212> DNA  
 <213> Arabidopsis thaliana

<400> 20  
 ccacgcgtcc gctccaccag aatttgtttt aggcctctct tcttctgttt ctttttctcc 60  
 caaagaaaca attagat 77

<210> 21  
 <211> 354  
 <212> DNA  
 <213> Arabidopsis thaliana

<400> 21  
 aaaagctcac gtcttttggt ctatcaaaaa tgtcacattg tcttttagctt tttgtagggg 60  
 gaaaaaaatg tttttttttt tgcaaagagt cttcagtttt ggtcagatca gagaattgtg 120  
 taccatgtta atcttaaacg cggtcgggaa ttggagtcgt gtgaaaacgc cgctgctgtt 180  
 gtttggtatg aatattatac aatagaattt gttgtcttac caaaaaaagt ctatgaagac 240  
 actgaagagc aaattattat ttttaagggg aaatttccaa aataaacttc atgtattcaa 300  
 aatttgcttg aaaaaacctc aatttttttt gttgaaaaaa aaaaaaaaaa aaaa 354

<210> 22  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:  
 oligonucleotide

<400> 22  
 cagaccacaa taccttcaaa aata 24

<210> 23  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:

oligonucleotide

<400> 23  
ccattgtgtc tccctccgc tggt

24

<210> 24  
<211> 5077  
<212> DNA  
<213> Arabidopsis thaliana

<400> 24  
atgattgtaa aacttgacag ggaggatgtt agtgatacac ttcgagtact tgttgcaact 60  
gattggcact tgggctacat ggagaaggat gaaattaggc ggcattgattc atttaaggct 120  
ttcgaagaga tatgttctat agctgaggag aaacaggctt ggtattcagt atctatccct 180  
tgccagtatt atcttgcggt tgaatcatct aacatattat cttaaataaa aatcttctcc 240  
caatattatg agtagtaaac agtgttctac ctaattttta caaaaattca accaattgctg 300  
aggaagaatt ctcagaaagt ttcatactct cttttttcac tcttttgaaa cagggtggact 360  
tcttactcct cggagggtgat ctttttcatg agaataaacc ctctagaact acggttagtta 420  
aagccattga aattcttctg cgccactgtc tgaatgataa accagtgcag tttcaagtag 480  
tcagcgacca gacagtaaat tttcagaatg cgtgagactc tatcctttct gctattaatc 540  
taatcataac aggaataat ttcaactgaa ctaattaatt ggcaaattgg ctcaaattcg 600  
tgtatagatt tacgtattct tattaatccc ttgacattat tttctggcta cagggttggg 660  
caagtcaatt acgaggatcc acacttcaat gtaggcttgc ccgtgttcag tattcatgga 720  
aaccatgatg atccagccgg agtggtacat cacttacatc tgcattgctct tgttatgcaa 780  
actcatttga ataggtatat agaactggat tagttagtga ataggtattt tattgtgttt 840  
ttgttctatg tctcttatgg ctacaggaca atctttctgc aattgatatt ctttccgcat 900  
gcaaccttgt gaactatttt ggaaagatgg ttcttggtgt tcttggtgtt ggccagatta 960  
ctctctaccc tatacttatg aagaaggttg gtgtaaagaa tttctaacct agacacctgg 1020  
ctccccctga cttcttgagc tatcatttaa tcaaattaat gtttagggct caacaaccgt 1080  
ggctctctat ggtttaggaa acatcaggga tgaacgtctc aatagaatgt ttcaggtaat 1140  
ccagaggacc ctacaccttt gctatacaat tgttaattgt gtttaatttt attggtttca 1200  
cagacccac atgctgtcca atggatgagg cctgaagttc aagaaggatg tgatgtttct 1260  
gactggttca acattctggg gcttcatcaa aatagggtga ttccattgct ataacatctt 1320  
ttagatcggt ttcttactca ttctgtatca gaaaatttga tactgtattc atatgacttg 1380  
cagggtgaaa tcaaaccaca aaaatgcaat aagtgcacac tttctccac gtttctcga 1440  
cttcatttgg tggggccatg agcatgaatg ctaaattcgac cccaggtcc atgaaaaatt 1500  
tgatttttgg agttattgca tttaaataag agtgagccac aatgttactt gcctctttga 1560  
gctaaaagct attaaacttt tgaaggaggt atctggaatg ggcttccaca tcacacaacc 1620  
aggatcttct gtggcaacat cacttattga tggggaatcg aagccaaaac atgttcttct 1680  
cttagaaatc aagggttcttc agcaaacaat ctgaaatttc atcttcactt tattcgact 1740  
tcattttctg gtcttttttc ctctttttca atcaagcatg taagcttgag tgacttaaaa 1800  
tatatgactt acagggaaat caatatcgtc ctacgaagat acccttgaca tctgtgaggc 1860  
cttttgagta tacagaggtta aagtttactt ttcttaata tgttatggtg gtggcagact 1920  
cttttgctta catattttca aagtcagat tgttttaaaag gatgaaagtg atattgatcc 1980  
caatgatcaa aactcaattc tggaaacatt ggataaagtg gtacctattc cctcttctca 2040  
tagttcatgt ggatatcttt tctcctgccc tttttgaata accagtcact gaatgtctct 2100  
actaatatct acaaaattgt taggtcagaa atctaataga gaaagctagc aaaaaagctg 2160  
ttaacagatc agagatcaaa ctcccattgg ttccaatcaa ggtaacttgt ttccaagttt 2220  
tcttcaaact gctgcaaatt ctagcaacac tcatataatt aaacctttat tttctaacc 2280  
aactctagag gctaggcttt gccagtttga tgcattgcaca cccatagcca caaacagata 2340  
attgttatta agaattattaa atgactgaca aaagactaag atctgcttca tctttcagg 2400  
agattattct ggatttatga cgataaatcc tcaaagattt ggacagaaat atgtgggaaa 2460  
ggtacctaga aattagttac tgaacatga tggtcaccat acttctttga atgttggtca 2520  
actaatgaca aagtccaaa cacttacagg ttgcaaatcc ccaggacatt ttgatatttt 2580  
ccaaggcttc taagaagggt cggagcgaag gtaagggcat tgggtgacta gtaatttata 2640  
caattttgtt tggattagat tgatgcacgt gcttttactc taacttgtaa tagcttatct 2700  
ggcaaaaatt acggttaagt agtgcattct agatatagta atgtagaaca atatgggcct 2760  
atgataacct ctttggttgt tttattgtcg gtattataat tctcgtcata tatatcatga 2820  
ctactaactt tctgttgtgt ggagcttgat attgatgtat tgagtgttaa ttttctttct 2880  
gttccacttt tcttgttata gttcatgttt cttcgtgtgt aacctatagc atcaaaattt 2940  
tgcgaatctt atggattatc tctagttagt atatatggga aatttgccat tttgataatt 3000  
tttttgtcta gtgaattgaa tggcaatgat gcatgtcctg atggttgtcc agtgatccag 3060  
ttatgatata tttcaatctt ccatttcaca gccaacatcg atgattctga gcggcttctg 3120

ccagaagaac	tgaaccagca	gaatatagaa	gcttttagtag	ctgaaagcaa	cctggtacat	3180
cctgcaacct	tctttcccta	tgattgtgtt	attatcgta	acccctgtag	aactttgcca	3240
cagaatgata	tagacttggg	tagttaccaa	atgggcatga	gtacactatg	ggatgatcat	3300
tctattttct	tccgcagaaa	atggagatcc	ttccagttaa	cgatctggat	gttgctcttc	3360
acaattttgt	gaacaaggat	gataaactag	ccttctactc	atgctgtcag	tacaatcttc	3420
aagagactcg	tgtatgtact	attttttact	tcaccattca	atacaaagtt	ctgcatagga	3480
tattattttt	atttcgtagc	acgtccttgt	tattgctttt	atgatttatc	tcttccctct	3540
ttttgtacag	ggtaaacttg	caaaggattc	agatgccaa	aaatttgagg	aagatgactt	3600
gattcttaaa	gtgggagagt	gcttagaggc	aagaagatat	agattcagtt	agttctgccg	3660
cagattatga	gaaccagcag	aattattgatc	tcacttgcat	tattgttcgt	gcaggaacgc	3720
ttgaaagata	ggtccactcg	acccactggt	tcctcacagt	ttttatccac	tggttgactt	3780
tcagagggtt	aaattctctt	tttttagattt	tccttgccct	tgctcttccg	ttggtttctc	3840
acagtgtctat	tttctacctg	agattggtac	agaatttgac	aaaaggaagc	agtggcatcg	3900
cgaatgcttc	gttcagtgat	gatgaagaca	caactcagat	gtctggttta	gctcctccca	3960
ctagaggacg	aagagggttca	tccactgcta	atacaactcg	tggtagagct	aaagcccca	4020
ccagaggacg	aggccgtggt	aaggccctcaa	gtgcgatgaa	gcaaaccact	cttgatagtt	4080
ctcttggttt	cgcgcagtct	caaaggtaac	tttttgacag	cacatttaac	cagtttaggg	4140
taggattcac	ggacgtgcaa	ggaaatgatt	ggcatcacta	gctagcta	gttatgtccc	4200
taatttgtct	ttcatagatc	tgcttcggct	gctgcttcag	ctgccttcaa	aagtgttcc	4260
accattggag	aagatgatgt	agattctcct	tcaagcgaag	aagtcgagcc	tgaagatttt	4320
aacaaacctg	acagcagttc	ggtatggact	attccttaca	ctgttattca	tttgttctc	4380
accataagaa	agcccattgta	aaaacttgac	aacatataac	ttttggcatt	cttatttctc	4440
tatttgaagt	aaattttg	tttttacttt	tcctgattct	tgtttgatat	ccactaaagg	4500
aggacgatga	gagcactaaa	ggcaaaggac	gtaaaagacc	agctactact	aagagaggca	4560
gaggtagagg	ttctgggact	tcaaaacgtg	gtagaaaaaa	cgaaagctct	tcttcaacta	4620
ataggctact	cagtagcaaa	gacgatgacg	aggacgaaga	tgatgaagac	agagaaaaga	4680
agcttaacaa	atctcagcct	cgggtttgtt	aatcacatct	attttccctt	ctttcgctgc	4740
ttattagcag	gttttagtaa	gttggtgtta	accatttgag	atcaaagctc	acttaatagt	4800
acaatttgaa	tatgcagggt	acaaggaact	atggagctct	aagaagataa	atacatatca	4860
aaccccaatc	tctgacatca	caacgaagct	tcatttttct	gttattttct	agcgacctct	4920
caagcggaac	aacttctgaa	gaagagaaat	tagtactaac	aagagttctg	tgagatgatg	4980
tacagagaat	tttgtagtgt	tttttttct	tgctcttttt	aaggttacgt	tggtgatgaa	5040
tgaggcaata	tgattaacgt	cagtaagaag	tctaaaa			5077

<210> 25

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:  
oligonucleotide

<400> 25

tgtaaaacga cggccagt

18

<210> 26

<211> 255

<212> DNA

<213> Arabidopsis thaliana

<400> 26

atacatatca	aaccccaatc	tctgacatca	caacgaagct	tcatttttct	gttattttct	60
agcgacctct	caagcggaac	aacttctgaa	gaagagaaat	tagtactaac	aagagttctg	120
tgagatgatg	tacagagaat	tttgtagtgt	tttttttct	tgctcttttt	aaggttacgt	180
tgttgatgaa	tgaggcaata	tgattaacgt	cagtaagaag	tctaaaaaaa	aaaaaaaaaa	240
aaaaaaaaaa	aaaaa					255

<210> 27

<211> 2935

<212> DNA

<213> Arabidopsis thaliana

<400> 27

tcatgcatga	actggcctag	caccagaaga	aagctgcaca	ttcgcggcat	attcacgtgc	60
ccacaagtca	tagtgaacaa	tctcttcaag	agacggtgat	gttaccaact	cgtttcgatg	120
tttatcgcat	gttaattcca	caaccttgaa	gatatccaaa	tagcttatcc	tgtaaacaaa	180
agtgagaata	taaacaattg	tgattcgtat	caagaacttc	attgagatgc	tcaaaactga	240
aaaataattc	ttacttttca	tcaatgaaca	tttcaacagc	tttctcattg	gcggcgctga	300
gaactccagt	cattgtgcct	ccagctcgtc	cagcagcata	agcaagatcc	atggatgggt	360
atttcacatt	gtctgggttc	ttgaaagtca	atgaaccgag	tctgccaaaa	tccacaattg	420
taaacaactt	ttgggttttag	gtgctgaatg	ctgatagata	aggcagtggg	cctaaccag	480
tttaactgat	ccacaccaa	acagtagcaa	aataaccaat	tgcaaaacca	aaccgaagac	540
cgattcgggt	tcatttttta	tcttatctaa	acaacctaaa	accaaactga	aaacaagatt	600
ggggaacttt	tcttggtgat	aattaaaatt	ttcaactaag	cttagcttca	cacttgataa	660
acagagagta	tataaatgtg	gttagcttac	ttgcaaagg	caagtcttgg	ccaagttact	720
tcagaacaag	gaactctatc	gggccatgac	atggtgtaga	gaatcggtaa	acgcatatca	780
ggccaaccca	attgagcaag	cacagatgaa	tcctgtggaa	caaaacaaat	acatgttata	840
cagttatttt	tttaaaaccg	gaaaaataat	aatttagtta	gtaatgtttc	agcaagacct	900
gtgtttcaat	catggaatgt	atgatacttt	gcggatgaat	gacaatctct	atatcgtcac	960
actcagctcc	aaacaaataa	tgcgcttcaa	tgacctcaag	accctgtttc	aaaaaatcaa	1020
gaactcatct	accttgatca	aaggattttt	caaaatcaga	gtttaacctt	aggagaaaa	1080
aatcttaacc	ttgttgaaaa	gcgtagcaga	gtccacagt	attttctttc	ccatgttcca	1140
gttttgatgc	ttcaacgcgt	ccgctacttt	aacttctctt	agcttttctga	caggccaatc	1200
cctttttcaa	aatccagtga	aaagtgttcca	ttaaccaaac	gagaattgag	aagaaaaaaa	1260
gtctatgcag	agagagaaga	atatcgaaac	aaacctaaaa	gtccaccag	atgcagtcaa	1320
gattatcttg	cgcagagcgc	cttcaggcaa	accttgaata	cactagagaa	cataaaagaa	1380
gatttttcac	tcaaattgcc	agaggttgaa	cttgcatata	gaccaacgct	gaactcaata	1440
tgaaagtgtg	ggtacttaat	tctatgtgat	ttgtgatacc	tgaaatatgg	cagaatgttc	1500
tgaatctgcc	ggaagaatct	ttacattatg	ttgtttggca	agcgggaagca	cgaaaggacc	1560
acctgcgatt	aatgtctctt	tggttgcaag	agcaatgtcc	tttcctgctt	caattgcagc	1620
aaacgtaggc	tgagtaaaaa	ataagcaaca	agctttatca	tctgcaactt	tcttttttca	1680
tatcctctta	ataaggttta	ataacaaaaa	attagagtat	atacctttag	tcccgacaaa	1740
cctactattc	cggtacaac	ggttacagct	tcaggatgtc	gggcaacctg	ttgatgaaca	1800
taataagtaa	aaacctatct	acactacaat	caaaactaac	aaatgaacta	acctcaatca	1860
ctccttgctc	tcctggaata	atctcgagtt	tatagtccaa	atcagctaaa	gcctctttta	1920
gctcattaat	cagtgaactc	tttctaacag	caaccaatgc	aggcttaaat	ctccttacct	1980
gccaccattc	aaaatagaat	cacagaacca	tactatagag	atttcttgag	attgcagaag	2040
caaaagccta	aaccagaacc	tgatttctct	ggtttgatct	gatacataac	gagttaatac	2100
tatcttgctt	atgatactac	cactgaactg	agaattaaac	tgaattccaa	gtggtctgaa	2160
tgacaaattg	gagagactca	atactaattt	ttttacaaat	gaagccaact	tacctgatca	2220
gcaagtagag	taacattcga	accagcagct	agagccacaa	ctctgaattt	gtcaggattc	2280
tcagccacaa	tatccaatgt	ctgcaaaatg	gaagttcttg	tcgataaaaa	tgatgcaaca	2340
ataactcagt	aagaaaaaaa	tatcattctt	ctatgagtct	agtcattcat	aagacaaact	2400
taaagtctgg	tcatactcaa	gaactgcaca	ataatgcctt	aatcgaaata	aaacctgagt	2460
gccaatagaa	ccagtagatc	caacgataga	gatgggtttt	ggtccatccc	aagattgacg	2520
aggcgctca	gggacagctc	tcccaggcca	tgctggagga	ggttggtgtt	gctgctgcac	2580
tttactgaa	cacttaacac	cttttccaaa	acctctccct	tgattcctcc	tcctcaaaact	2640
aaaccacct	gtgaaacact	ccaaagatgt	aaaattttaa	actctacgac	ctaaagcaaa	2700
ccaaaaaaa	tcgaattgaa	gaaataacag	attacctaga	tagagaaatt	cacaagagcc	2760
taagacaact	aatgaaagtt	tgcaacttta	atcgaaaaga	gagttgacca	aggaggagga	2820
aagaagagag	gaagaagaag	aaacctgaga	gttttagggat	tggattgaac	ctggagggtat	2880
ccaagaaaga	aatagctttg	gattcagctg	gagatagtga	gtttaatgtc	atcat	2935

<210> 28

<211> 1434

<212> DNA

<213> Arabidopsis thaliana

<220>

<221> misc\_feature

<222> (1)..(1434)

<223> y = t or c



```

<400> 28
atgatgacat taaactcact atctccagct gaatccaaag ctatttcttt cttggatacc 60
tccaggttca atccaatccc taaactctca ggtgggttta gtttgaggag gaggratcaa 120
gggagaggtt ttggaaaagg tggttaagtgt tcagtgaag tgcagcagca acaacaacct 180
cctccagcat ggcctgggag agctgtycct gaggcgcctc gtcaatcttg ggatggacca 240
aaacccatct ctatcgttgg atctactggt tcyatyggca ctcagacatt ggatattgtg 300
gctgagaatc ctgacaaatt yagagttgtg gctctagctg ctggttcgaa tgttactcta 360
cttgctgatac aggtaaggag atttaagcct gcrttggttg ctggttagaaa cgagtcactg 420
attaatgagc ttaaagaggc tttagctgat ttggactata aacycgagat tattccagga 480
gagcwaggag tgattgaggt tgcccgcacat cctgaagctg taaccgttgt taccggaata 540
gtaggttgtg cgggactgma gcctacgggt gctgcaattg aagcaggaaa ggacattgct 600
cttgcaaaca aagagacatt aatcgcaggt ggtcctttcg tgcttccgct tgccaacaaa 660
cataatgtaa agattcttcc ggcagattca gaacattctg ccatatttca gtgtattcaa 720
ggtttgctcg aaggcgctct gcgcaagata atcttgactg catctggttg agcttttagg 780
gattggcctg tcgaaaagct aaaggaagtt aaagtagcgg atgcgttgaa gcatccaaac 840
tggaacatgg gaaagaaaat cactgtggac tctgctacgc ttttcaacaa gggctcttgag 900
gtcattgaag cgcattatct gtttgagct gagtatgacg atatagagat tgtcattcat 960
cckcaaagta tcatacattc catgattgaa acacaggatt catctgtgct tgctcaattg 1020
ggttggcctg atatgcggtt accgattctc tacaccatgt catggcccga tagagttcct 1080
tgttctgaag taacttggcc wagacttgac ctttgcaaac tcggttcatt gactttcaag 1140
aaaccagaca atgtgaaata cccatccatg gatcttgctt atgctgctgg acgagctgga 1200
ggcacaatga ctggagttct cagcgccgcc aatgagaaag ctggtgaaat gtttattgat 1260
gaaaagataa gctatttggg tatcttcaag gttgtggaat taacatgcga taaacatcga 1320
aacgagttgg taacatcacc gtctcttgaa gagattgttc actatgactt gtgggcacgt 1380
gaatatgccg cgratgtgca gctttcttct ggtgctaggc cagttcatgc atga 1434

```

```

<210> 29
<211> 477
<212> PRT
<213> Arabidopsis thaliana

```

```

<220>
<221> SITE
<222> (39)
<223> Xaa = Asp or Asn

```

```

<220>
<221> SITE
<222> (155)
<223> Xaa = Pro or Leu

```

```

<220>
<221> SITE
<222> (162)
<223> Xaa = Leu or Gln

```

```

<220>
<221> SITE
<222> (187)
<223> Xaa = Lys or Gln

```

```

<220>
<221> SITE
<222> (465)
<223> Xaa = Asp or Asn

```

```

<400> 29
Met Met Thr Leu Asn Ser Leu Ser Pro Ala Glu Ser Lys Ala Ile Ser
  1              5              10              15
Phe Leu Asp Thr Ser Arg Phe Asn Pro Ile Pro Lys Leu Ser Gly Gly
          20              25              30

```

Phe Ser Leu Arg Arg Arg Xaa Gln Gly Arg Gly Phe Gly Lys Gly Val  
35 40 45  
Lys Cys Ser Val Lys Val Gln Gln Gln Gln Gln Pro Pro Pro Ala Trp  
50 55 60  
Pro Gly Arg Ala Val Pro Glu Ala Pro Arg Gln Ser Trp Asp Gly Pro  
65 70 75 80  
Lys Pro Ile Ser Ile Val Gly Ser Thr Gly Ser Ile Gly Thr Gln Thr  
85 90 95  
Leu Asp Ile Val Ala Glu Asn Pro Asp Lys Phe Arg Val Val Ala Leu  
100 105 110  
Ala Ala Gly Ser Asn Val Thr Leu Leu Ala Asp Gln Val Arg Arg Phe  
115 120 125  
Lys Pro Ala Leu Val Ala Val Arg Asn Glu Ser Leu Ile Asn Glu Leu  
130 135 140  
Lys Glu Ala Leu Ala Asp Leu Asp Tyr Lys Xaa Glu Ile Ile Pro Gly  
145 150 155 160  
Glu Xaa Gly Val Ile Glu Val Ala Arg His Pro Glu Ala Val Thr Val  
165 170 175  
Val Thr Gly Ile Val Gly Cys Ala Gly Leu Xaa Pro Thr Val Ala Ala  
180 185 190  
Ile Glu Ala Gly Lys Asp Ile Ala Leu Ala Asn Lys Glu Thr Leu Ile  
195 200 205  
Ala Gly Gly Pro Phe Val Leu Pro Leu Ala Asn Lys His Asn Val Lys  
210 215 220  
Ile Leu Pro Ala Asp Ser Glu His Ser Ala Ile Phe Gln Cys Ile Gln  
225 230 235 240  
Gly Leu Pro Glu Gly Ala Leu Arg Lys Ile Ile Leu Thr Ala Ser Gly  
245 250 255  
Gly Ala Phe Arg Asp Trp Pro Val Glu Lys Leu Lys Glu Val Lys Val  
260 265 270  
Ala Asp Ala Leu Lys His Pro Asn Trp Asn Met Gly Lys Lys Ile Thr  
275 280 285  
Val Asp Ser Ala Thr Leu Phe Asn Lys Gly Leu Glu Val Ile Glu Ala  
290 295 300  
His Tyr Leu Phe Gly Ala Glu Tyr Asp Asp Ile Glu Ile Val Ile His  
305 310 315 320  
Pro Gln Ser Ile Ile His Ser Met Ile Glu Thr Gln Asp Ser Ser Val  
325 330 335  
Leu Ala Gln Leu Gly Trp Pro Asp Met Arg Leu Pro Ile Leu Tyr Thr  
340 345 350  
Met Ser Trp Pro Asp Arg Val Pro Cys Ser Glu Val Thr Trp Pro Arg  
355 360 365  
Leu Asp Leu Cys Lys Leu Gly Ser Leu Thr Phe Lys Lys Pro Asp Asn  
26

370

375

380

Val Lys Tyr Pro Ser Met Asp Leu Ala Tyr Ala Ala Gly Arg Ala Gly  
 385 390 395 400

Gly Thr Met Thr Gly Val Leu Ser Ala Ala Asn Glu Lys Ala Val Glu  
 405 410 415

Met Phe Ile Asp Glu Lys Ile Ser Tyr Leu Asp Ile Phe Lys Val Val  
 420 425 430

Glu Leu Thr Cys Asp Lys His Arg Asn Glu Leu Val Thr Ser Pro Ser  
 435 440 445

Leu Glu Glu Ile Val His Tyr Asp Leu Trp Ala Arg Glu Tyr Ala Ala  
 450 455 460

Xaa Val Gln Leu Ser Ser Gly Ala Arg Pro Val His Ala  
 465 475